805,20

#### ✓ STIC-Biotech/ChemLib

Bowman, Amy

Sent: Monday, May 01, 2006 5:09 AM

To: STIC-Biotech/ChemLib
Cc: Bowman, Amy

Subject: sequence search-SEQ ID 82

Hello,

From:

I need a search of SEQ ID NO: 82 in application 10/605,498, length limited to 35 nucleotides. I need to include an interference search.

Thank you, Amy Bowman AU 1635 REM 2C31 mail REM 2C18 571-272-0755

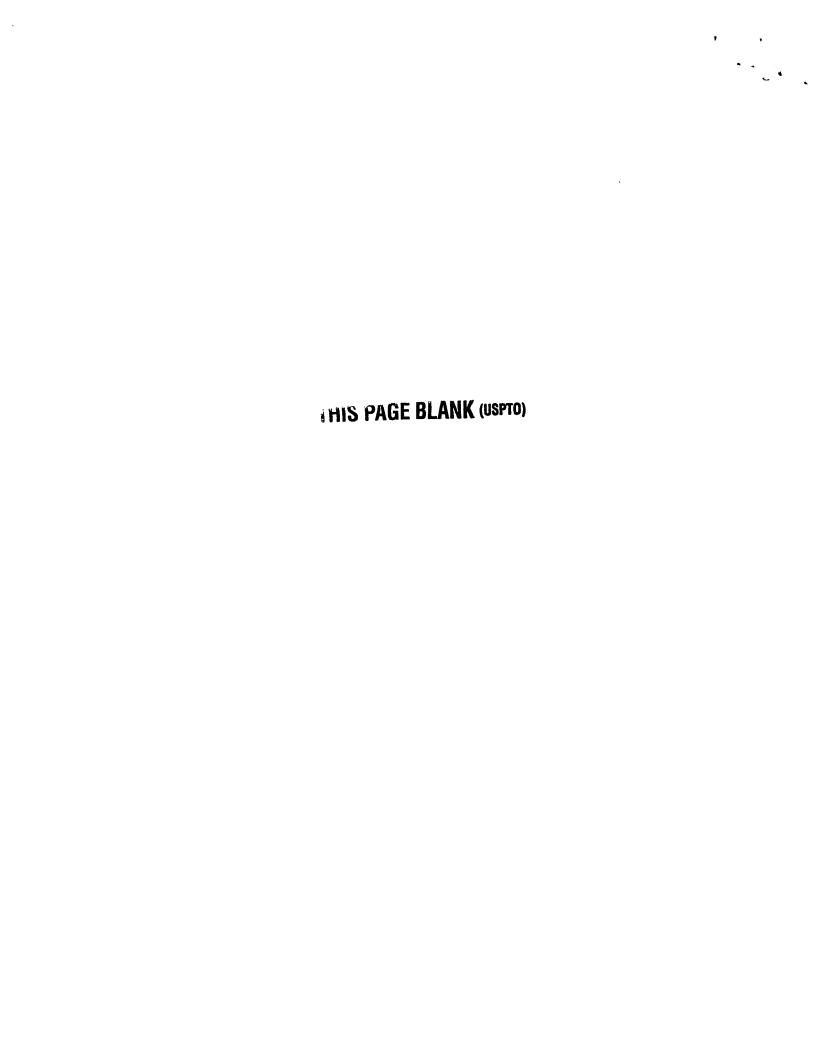
Searcher Phone: 2250 Y
Date Searcher Picked up: 518104
Date completed: 518104
Searcher Prep Time: 10
Online Time: 10

Type-of Search
NA#\_\_\_\_\_ AA#:\_\_\_\_
S/L:\_\_\_\_ Oligomer:\_\_\_\_\_
Encode/Transl:\_\_\_\_ Text:\_\_\_
Inventor:\_\_\_\_ Litigation:\_\_\_

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*
Vendors and cost where applicable STN:\_\_\_\_\_\_
DIALOG:\_\_\_\_\_\_

QUESTEL/ORBIT:
LEXIS/NEXIS:

SEQUENCE SYSTEM: WWW/Internet: Other (Specify):



Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

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OM nucleic

Run on:

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PAT 28-APR-2004
                 AR235594 Sequence
BD010384 Chimeric
CQ816314 Sequence
CQ816319 Sequence
CQ818995 Sequence
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AX445408 Sequence
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AX45796 Sequence
BD235548 Methods a
AX16265 Sequence
AX30545 Sequence
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AX31064 Sequence
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AX11068 Sequence
AX12189 Sequence
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AX13064 Sequence
AX213189 Sequence
AX213425 Sequence
AX21851 Sequence
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
 92 Sequence
Sequence 9
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Jeave,M.E., Rocchi,P. and Signaevsky,M.
Compositions for treatment of prostate and other cancers
Patent: WO 2004030660-A 82 15-APR-2004;
The University of British Columbia (CA)
Location/Qualifiers
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Pred. No. 9.7e+02;
Mismatches 0; Indels
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Sequence 81 from Patent WO2004030660.
CQ799983.1 GI:46848930
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Sequence 82 from Patent WO2004030660.
CQ799984.1 GI:46848931

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AR235394
AR235394
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CQ816319
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CQ818829
CQ818820
CQ81820
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AX461824
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Homo sapiens (human)
 Hominidae; Homo
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                 DEFINITION
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JOURNAL
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CQ799984
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CQ799983
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CQ799992 Sequence
CQ799905 Sequence
CQ799906 Sequence
AX559501 Sequence
AX473165 Sequence
B41696 Process for
AX44276 Sequence
BD243529 Nucleotid
AX034952 Sequence
AX64030 Sequence
AX64030 Sequence
AR579704 Sequence
                                                         8, 2006, 09:18:02 ; Search time 1773 Seconds (without alignments) 641.212 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
       5.1.8
Biocceleration Ltd.
                                                                                                                                                                                1770318
                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                             5883141 segs, 28421725653 residues
       GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                          Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          nucleic search, using sw model
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CQ799983
CQ799905
CQ799905
CQ799906
AR5473165
E41696
AR454276
AR454276
AX684030
AR579704
AR529809
AR528809
AR363940
                                                                                                                 gggacgcgctcggtcat 20
                                                                                                                                 IDENTITY NUC.
Gapop 10.0 , Gapext 1.0
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seq length: 35
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Gaps

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PAT 28-APR-2004

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL Bource

ORIGIN

FEATURES

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Unclassified.
1 (basssified.
1 (basss 1 to 33)
Summers, A.O. and Caguiat, J.J.
Metal binding proteins, recombinant host cells and methods
Patent: US 6750042-A 16 15-JUN-2004;
University of Georgia Research Foundation, Inc.; Athens, GA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gleave, M.E., Rocchi, P. and Signaevsky, M.
Compositions for treatment of prostate and other cancers
Patent: WO 2004030660-A 15-APR-2004;
The University of British Columbia (CA)
Location/Qualifiers
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  Patent: WO 2004030660-A 3 15-APR-2004;
The University of British Columbia (CA)
Location/Qualifiers
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Seguence 4 from Patent WO2004030660.
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6750042.
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

    .33
/organism="unknown"
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AR559501
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Matches 16; Conserv
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KEYWORDS
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AUTHORS
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CQ799906
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                                             FEATURES
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Compositions for treatment of prostate and other cancers
Patent: WO 2004030660-A 90 15-APR-2004;
The University of British Columbia (CA)
Location/Qualifiers
                                                                                                 Gleave, M.E., Rocchi, P. and Signaevsky, M.
Compositions for treatment of prostate and other cancers
Patent: WO 2004030660-A 81 15-APR-2004;
The University of British Columbia (CA)
Location/Qualifiers
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100.0%; Score 20; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Sequence 90 from Patent WO2004030660.
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Sequence 3 from Patent WO2004030660.
CQ799905.
CQ799905.1 GI:46848852
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DEFINITION ACCESSION VERSION

CQ79992/c

LOCUS

RESULT 3

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

JOURNAL

Bource

ORIGIN

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PAT 08-OCT-2004

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

DEFINITION

RESULT 4 CQ799905

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C12N15/09, C12Q1/68, C12N15/00
Nucleotide fragment, probe, primer, reagent, and method for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric plant promoters comprising sugar-regulatory sequences Patent: US 6680425-A 19 20-JAN-2004; The Regents of the University of California; Oakland, CA Location/Qualifiers
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.6e+05;
Matches 13; Conservative 0; Mismatches 0;
                                                                  66.0%; Score 13.2; DB 6;
83.3%; Pred. No. 5.2e+05;
ive 0; Mismatches 3;
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Sequence 19 from patent US 6680425.
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JP 2002537856-A/36
12-NOV-2002
03-MAR-2000 JP 2000603424
05-MAR-1999 FR 99/02968
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/organism="unknown"
/mol_type="genomic DNA"
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JP 2002537856-A/36.
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                                                               Query Match
Best Local Similarity 83.3
Matches 15; Conservative
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Rodriguez, R.L.
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BD243529/c
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CIZN15/09, CIZN1/21, CIZP13/14// (CIZN1/21, CIZR1:15), (CIZP13/14,
CIZR1:15),
CIZN15/00
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Metal binding proteins, recombinant host cells and methods
Patent: WO 0230962-A 16 18-APR-2002;
UNIVERSITY OF GEORGIA RESERRCH FOUNDATION, INC. (US)
Location/Qualifiers
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E41696
E41696.1 GI:18633367
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/organism='Artificial Sequence'.
Location/Qualifiers
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Pred. No. 2e+05;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                   DNA
         Pred. No. 2e+05;
0; Mismatches
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Sequence 16 from Patent WO0230962.
AX473165
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Best Local Similarity 84.2%;
Matches 16; Conservative (
   84.2%;
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Best Local Similarity 84.2
Matches 16; Conservative
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cother sequences, artificial sequences.

cother sequences; artificial sequences.

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Emaux, P.G., Cho, M.J. and Buchanan, R.B.

Production of proteins in plant seeds
Artificial Sequence

No Artificial Sequence
No Artificial Sequence
No SEP-1998 JP 2000513959

PR 30-SEP-1997 US 60/060510

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Production of proteins in plant seeds

Patent: US 6642437-A 12 04-NOV-2003;

The Regents of the University of California; Oakland,

Location/Qualifiers
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/organism='Artificial Sequence'
Location/Qualifiers
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     Pred. No. 7.8e+05;
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    .24
    forganism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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/organism="unknown"
/mol_type="genomic DNA"
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JP 2001518305-A/10.
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synthetic construct
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     Best Local Similarity 87.5
Matches 14; Conservative
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AUTHORS
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AUTHORS
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KEYWORDS
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Patent: WO 03006502-A 3 23-JAN-2003;
Exclixis Deutschland GMDH (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        PAT 15-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT 29-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclectide fragment, probe, primer, reagent and method for detecting a nuclectide sequence derived from pbr322 replication
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                                                                                                                                                           Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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/mol_type="unassigned DNA"
/db_xref="taxon:47470"
                                                                                                                                                   Query Match
64.0%; Score 12.8; DB 6;
Best Local Similarity 87.5%; Pred. No. 7.8e+05;
Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 64.0%; Score 12.8; DB 6; Similarity 87.5%; Pred. No. 7.8e+05; 14; Conservative 0; Mismatches 2;
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LAMY DIDIER (FR); TRANSGENE (FR)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                  AX034952 23 bp
Sequence 36 from Patent WO0053803.
AX034952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AX684030 24 bp
Sequence 3 from Patent WO03006502.
AX684030
1. .23
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AX034952.1 GI:11190877
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Cloning vector pBR322
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Best Local Similarity
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

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RESULT 11 AX034952/c

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Query Match

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

DEFINITION

RESULT 12 AX684030 LOCUS

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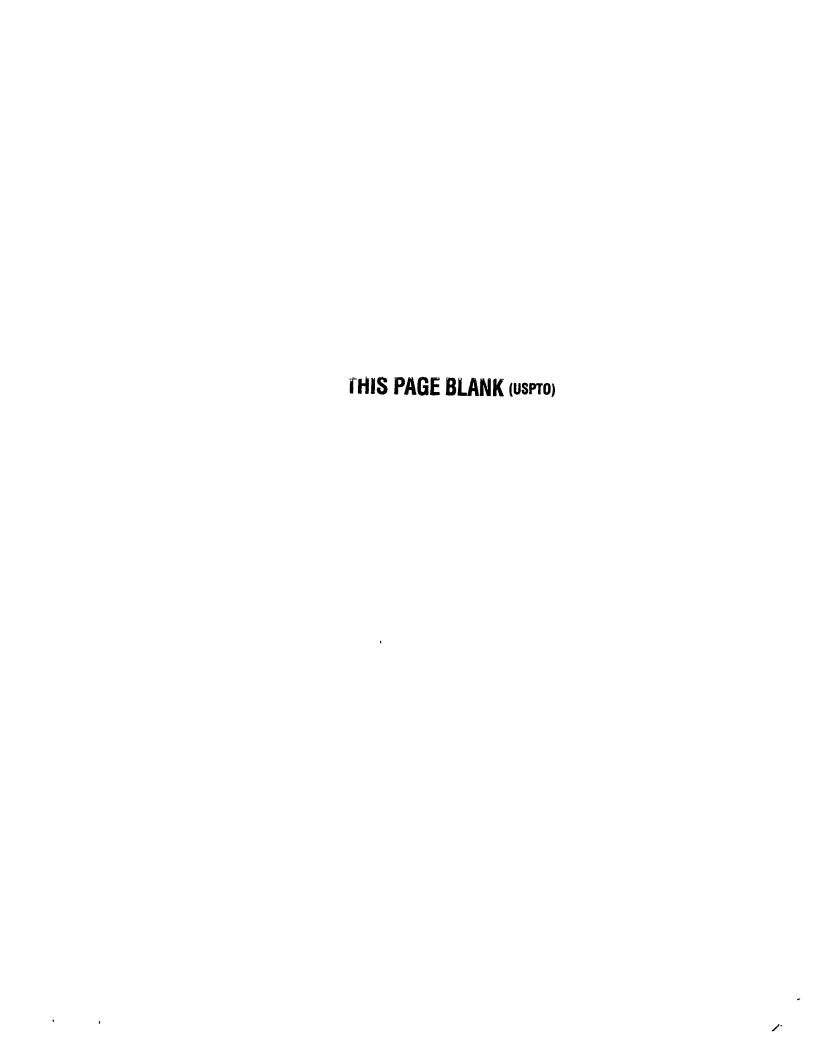
Matches

ORIGIN

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Unknown.
Unknown.
Unknown.
Unclassified.
CE 1 (bases 1 to 24)
RS Cho,M.-J., Lemaux,P.G., Buchanan,B.B., Wong,J. and Marx,C.
RO,M.-J., Lemaux,P.G., Buchanan,B.B., Wong,J. and Marx,C.
RAL Patent: US 6784346-A 14 31-AUG-2004;
The Regents of the University of California; Oakland, CA
Location/Qualifiers
Source / Organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                                     PAT 14-DEC-2004
    Gaps
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   4; Indels
                                                                                                                                     DNA
 0; Mismatches
                                                                                                                                  AR579704 24 bp D
Sequence 14 from patent US 6784346.
AR579704
AR579704.1 GI:56583159
                               2 GGACGCGCCCTCGGTCAT 20
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                                               | ||| |||||||| ||
19 GCACGAGGCGCTCGGATAT 1
 15; Conservative
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AR579704/c
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Matches
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Search completed: May 8, 2006, 09:47:45 Job time : 1776 secs



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8, 2006, 09:56:51; Search time 602 Seconds (without alignments) 274.730 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
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GenCore version 5.1.8 Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9793542 seqs, 4134689005 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                        OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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20
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query	1		SUMMARIES	;
Q i	score	Match	Length DB	90	ID	Description
	1 20	100.0	20	7	US-10-605-498-82	Sequence 82, Appl
	2 20	100.0	21	7	US-10-605-498-81	Sequence 81, Appl
υ	3 19	95.0	19	7	US-10-605-498-90	90
•	4 16	80.0	21	7	US-10-605-498-3	3,
ט	5 15.2	76.0	25	7	US-10-719-956-135321	13
_	9	75.0	21	7	US-10-605-498-4	Sequence 4, Appli
	7 14.2	71.0	25	10	US-11-036-317-261850	
-	8 14.2	71.0	25	10	US-11-036-317-269817	Sequence 269817,
	9 14.2	71.0	25	10	US-11-036-317-330516	Sequence 330516,
ā	0 14.2	71.0	25	10	US-11-036-317-332488	Sequence 332488,
-		71.0	25	10	US-11-036-317-364465	Sequence 364465,
-	2 14.2	71.0	25	10	US-11-036-317-406575	Sequence 406575,
ī	3 14.2	71.0	25	10	US-11-036-317-536426	Sequence 536426,
ä		71.0	25	10	US-11-036-317-536427	Sequence 536427,
ਜ	5 14.2	71.0	33	m	US-09-977-137A-16	Sequence 16, Appl
ਜ	6 14	70.0	25	Ŋ	US-10-215-112-7242	Sequence 7242, Ap
-	7 14	70.0	25	σ	US-10-809-189-42173	-
-		0.69	25	σ	US-10-809-189-46323	Sequence 46323, A
o Fi	9 13.8	69.0	25	σ	US-10-809-189-46324	Sequence 46324, A
ō U	0 13.8	0.69	25	σ	US-10-809-189-46335	Sequence 46335, A
0	13.6	68.0	25	7	US-10-719-956-135322	Seguence 135322,
6	2 13.6	68.0	25	7	US-10-719-956-198103	Sequence 198103,
	3 13.6	68.0	25	æ	US-10-719-900-309243	Sequence 309243,

Sequence 912027,	Sequence 912041,	Sequence 3853, Ap	Sequence 65789, A	Sequence 110491,	Sequence 547822,	Sequence 547823,	Sequence 148603,	Sequence 849503,	Sequence 849504,	Sequence 53301, A	Sequence 321539,	Sequence 787134,	Sequence 166335,	Sequence 166384,	Sequence 229339,	Sequence 229340,	Seguence 19, Appl	Sequence 632447,	Sequence 883329,	Sequence 937963,	Sequence 3, Appli
US-11-036-317-912027	US-11-036-317-912041	US-10-098-263B-3853	US-10-098-263B-65789	US-10-719-956-110491	US-10-719-956-547822	US-10-719-956-547823	US-10-719-900-148603	US-10-719-900-849503	US-10-719-900-849504	US-10-809-189-53301	US-11-036-317-321539	US-11-036-317-787134	US-11-060-756-166335	US-11-060-756-166384	US-11-060-756-229339	US-11-060-756-229340	US-10-206-654-19	US-10-719-956-632447	US-11-036-317-883329	US-11-036-317-937963	US-10-193-692-3
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25	25	25	25	52	25	25	25	25	25	25	25	25	25	25	25	25	50	25	25	25	24
68.0	68.0	0.99	0.99	0.99	0.99	0.99	0.99	0.99	66.0	0.99	0.99	0.99	0.99	0.99	0.99	0.99	65.0	65.0	65.0	65.0	64.0
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24	25	c 26	27	28	c 29	c 30	31	32	33	34	35	36	c 37	38	G 33	c 40	41	42	43	44	45

# ALIGNMENTS

US-10-605-498-82

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APPLICANT: Gleave, Martin
APPLICANT: Gleave, Martin
APPLICANT: Gleave, Martin
APPLICANT: Signaevsky, Maxim
TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
TITLE OF INVENTION: Cancers
TITLE OF INVENTION: Cancers
TITLE OF INVENTION: Cancers
CURRENT APPLICATION NUMBER: US/10/605,498
CURRENT PILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,859
PRIOR APPLICATION NUMBER: US 60/463,952
PRIOR APPLICATION NUMBER: US 60/463,952
PRIOR APPLICATION NUMBER: 302-04-18
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MS-10-605-498-81
Sequence 81, Application US/10605498
Sequence 81, Sequence 82, Sequence 82, Sequence 82, Sequence 83, Sequence 84, Sequence 86, Sequence 87, Sequence 88, Seq
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Pred. No. 5.5;
Mismatches 0; Indels
; Sequence 82, Application US/10605498; Publication No. US20040127441A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Sco
100.0%; Pre
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Best Local Similarity
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LENGTH: 20
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Sequence 4, Application US/10605498;
Sequence 4, Application US/10605498;
Publication No. US20040127441A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gleave, Martin
APPLICANT: Signaev8ky, Maxim
TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
TITLE OF INVENTION: Cancers
FILE REFERENCE: UBC.P-031
CURRENT APPLICATION NUMBER: US 60/415,859
FRIOR APPLICATION NUMBER: US 60/415,859
PRIOR APPLICATION NUMBER: US 60/463,952
PRIOR APPLICATION NUMBER: US 60/463,952
PRIOR FILING DATE: 2003-04-18
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn version 3.2
SEQ 10 NO 4
LENGTH: 21
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xue Mei Zhou
TITLE OP INVENTION: Methods of Genetic Analysis of Rat
FILE REPRENCE: 3527.
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT PILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR APPLICATION NUMBER: 60/427,836
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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                                                                                                                                                                                                     DB 7; Le
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Pred. No. 1.2e+03;
0; Mismatches 3;
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                                                                                                                                                                                                  Query Match
80.0%; Score 16; DB
Best Local Similarity 100.0%; Pred. No. 4.9
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-719-956-135321/c
; Sequence 135321, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 GGGACGCAACGCTCGGCCAT 6
         NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin version 3.2
SEQ ID NO 3.2
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                             1 CGCGCGCTCGGTCAT 16
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85.0%;
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; ORGANISM: Rattus norvegicus
US-10-719-956-135321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.03
Matches 17; Conservative
                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-10-605-498-3
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US-10-605-498-4
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Best Local Similarity
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LENGTH: 25
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Publication No. US20040127441A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Gleave, Martin
APPLICANT: Rocchi, Palma
APPLICANT: Cancers
FILE REFERENCE: UBC.P-031
CURRENT APPLICATION NUMBER: US 60/415,859
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-18
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin version 3.2
SEQ ID NO 90
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10605498
Publication No. US20040127441A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Gleave, Martin
APPLICANT: Signawevsky, Maxim
APPLICANT: Signawevsky, Maxim
APPLICANT: Signawevsky, Maxim
APPLICANT: Signawevsky, Maxim
APPLICANT: Group Sitions and Methods for Treatment of Prostate and Other
TITLE OF INVENTION: Cancers
FILE REFRENCE: USC.P-011
CURRENT APPLICATION NUMBER: US/10/605,498
CURRENT APPLICATION NUMBER: US 60/415,859
PRIOR APPLICATION NUMBER: US 60/463,952
PRIOR PILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-04-18
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100.0%; Score 20; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 20; Conservative 0; Mismatches 0; Indels
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17;
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                   PRIOR APPLICATION NUMBER: US 60/415,859
PRIOR FILING DATE: 2002-10-02
PRIOR PPLICATION NUMBER: US 60/463,952
PRIOR PILING DATE: 2003-04-18
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin version 3.2
LENGTH: 21
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CURRENT FILING DATE: 2003-10-02
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-605-498-3
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TYPE: DNA
ORGANISM: Mus musculus
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US-11-036-317-332488
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LENGTH: 25
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TILLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 261850
LENGTH: 25
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE REFERENCE: 3654.11
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT PILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SSG ID NO 269817
LENGTH: 25
LENGTH: 25
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   Indels
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Pred. No. 3.6e+03;
0; Mismatches 3;
   Mismatches
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Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 269817, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
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84.2%;
                                                           GGACGCGCCTCG 21
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Best Local Similarity 84.2
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mus musculus US-11-036-317-261850
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US-11-036-317-269817
                                                                                                                                                  11-036-317-261850
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 15;
Matches
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US-11-036-317-364465

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(URREAL INFORMATION:

(URRENT Blume, John

(URRENT PILING DATE: 2005-01-13

(URRENT FILING DATE: 2005-01-13

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(URRENT PILING DATE: 2004-01-13

(URRENT FILING DATE: 2004-01-13

(URRENT PILING DAT
TITLE OF INVENTION: Wethod of Analysis of Alternative Splicing in Mouse FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR RPPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 330516
LENGTH: 25
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Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION:
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
FRIOR APPLICATION NUMBER: US 60/536,639
FRIOR PELICATION NUMBER: US 60/536,639
FRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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Pred. No. 3.6e+03;
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84.2%;
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Best Local Similarity 84.2
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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CORGANISM: Mus musculus
US-11-036-317-330516
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FEATURE:
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Sequence 536426, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Williams, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2004-01-13

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: History, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 365-01
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR PAPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 406575
LENGTH: 25
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                                       71.0%; Score 14.2; DB 10;
84.2%; Pred. No. 3.6e+03;
live 0; Mismatches 3;
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                                                                                                                                                                                                                                                                            Sequence 406575, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
                                                                                                                            1 GGGACGCGCGCTCGGTCA 19
                                                                                                                                                       4 GGGACGCGCGATCTGCCA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                           Best Local Similarity 84.2
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Mus musculus
US-11-036-317-406575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus
US-11-036-317-536426
US-11-036-317-364465
                                                                                                                                                                                                                                                      US-11-036-317-406575
                                          Query Match
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RESULT 14 US-11-036-317-536427

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; Sequence 536427, Application US/11036317; Publication Wo. US20050214823A1; Ebublication Wo. US20050214823A1; GENERAL INFORMATION: APPLICANT: Williams, Alan APPLICANT: Williams, John TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse; FILE REFERENCE: 3654.1 CURRENT APPLICATION NUMBER: US/11/036,317; CURRENT FILING DATE: 2005-01-13; PRIOR APPLICATION NUMBER: US 60/536,639; PRIOR PLING DATE: 2004-01-13; NUMBER OF SEQ ID NOS: 991174; SOFTHARE: Microarray Probe Sequence Listing Generator V 1.1; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-09-97-137A-16
US-09-977-137A-16
Sequence 16, Application US/09977137A
Sequence 16, Publication No. US2003104524A1
Seture 10 No. US2003104465
Seture 10 No. US2003104465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.2; DB 10;
Pred. No. 3.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.0%; Score 14.2; DB 3; Best Local Similarity 84.2%; Pred. No. 3.4e+03; Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: May 8, 2006, 10:41:19
Job time : 602 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGACGCGCGCCTCGGTCA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 GGGACGTGGCGCTTTGTCA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.0%;
84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.2.
                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-536427
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Title: Perfect score:

Sequence:

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OM nucleic

Run on:

Scoring table:

Searched:

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Minimum I Maximum

Database

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Ab196187 Primer #3
Aav44737 Pluoresce
Ad005568 Primer fo
Ad005568 Pluoresce
Ad40594 Human Arp
Aaq36810 Oligomer
Aav3686 PCR prime
Aav3680 PCR prime
Aav3601 Plasmid p
Ad73001 Probe rel
Adv71639 Plasmid p
Ad73001 Probe rel
Adv71639 Plasmid p
Ad73001 Probe rel
Adv3801856 Oligonucl
Ad038138 HIV envel
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Ad038105 HIV envel
Ad038105 HIV envel
Ad038105 HIV envel
                Aad59639 Bar ampli
Ad886174 PCAV-deri
Aac61525 PCR prime
Aac62482 Wheat thi
                                                                                                                                                                                                                                                                           Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:82.
                                                                                                                                                                                                                                                                                        shock protein 27; hsp27; cytostatic; gene therapy; shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
                                                                                                                                                                                                 ALIGNMENTS
                           ABL96187
AAV44737
AAV44737
AAV38854
ABA35882
AAAA0594
AAQ36810
AAQ36810
AAQ36805
AAV35805
AAV35805
AAV15301
ABQ71639
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ADO38185
ADO38102
ADO38074
                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                       antisense oligonucleotide; ss.
 ADM94732 standard; DNA; 20
                                                                                                                                                                                                                                                              (first entry)
 01-JUL-2004
ADM94732;
                                                                                                                                                                                                                                                                                         heat
heat
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                                                                                                                                                                                                                            ADM94732
 טטטט
                                             GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                         4393292
                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                          4996997 seqs, 3332346308 residues
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Maximum Match 100%
Listing first 45 summaries
                                nucleic search, using sw model
                                                                                        gggacgcgcgctcggtcat 20
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Gapop 10.0 , Gapext 1.0
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20
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seq length: 35
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11:
12:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adm94732 Human hea	Adm94731 Human hea	Adm94740 Human hea	Adm94653 Human hea	Adm94654 Human hea	Abk52211 Synthetic	Ach58106 DNA targe	Aci03862 Human mic	Aci65798 Human mic	Aah21740 Corynebac	Aav51704 Zea mays	Aaa75395 Fragment	Abz58873 Zebrafish	Aci84537 Human mic	Ado31537 Human CFT	Ady40845 PCR fragm	Abz08781 Human CMV	Acd26306 Bar assoc	Aax34633 Bar gene
SUMMARIES	ID	ADM94732	ADM94731	ADM94740	ADM94653	ADM94654	ABK52211	ACH58106	ACI03862 ,	ACI65798	AAH21740	AAV51704	AAA75395	ABZ58873	ACI84537	AD031537	ADY40845	ABZ08781	ACD26306	AAX34633
	DB	12	12	12	12	12	9	0	0	σ	4	7	٣	80	0	12	14	9	10	8
	Query Match Length DB	20	21	19	21	21	33	25	25	25	27	21	23	24	25	29	30	20	22	24
di	Query Match	100.0	100.0	95.0	80.0	75.0	71.0	70.0	0.99	0.99	0.99	64.0	64.0	64.0	64.0	64.0	64.0	63.0	63.0	. 63.0
	Score	20	20	19	16	15	14.2	14	13.2	13.2	13.2	12.8	12.8	12.8	12.8	12.8	12.8	12.6	12.6	12.6
	Result No.		7	n U	4	Ŋ	v	7	υ Θ	6	10	c 11	c 12	13	.c 14	15	16	17	18	c 19

ŏ New composition comprising a therapeutic agent that reduces the amount of active hsp27 in hsp27 expressing cells exposed to the therapeutic agent, useful in treating cancer, e.g., prostate cancer or a central nervous Claim 6; SEQ ID NO 82; 38pp; English. Ξ Signaevsky (UYBR-) UNIV BRITISH COLUMBIA Rocchi P, WPI; 2004-316331/29. system malignancy. Gleave ME, 

02-OCT-2003; 2003WO-CA001588. 02-OCT-2002; 2002US-0415859P. 18-APR-2003; 2003US-0463952P.

WO2004030660-A2

15-APR-2004.

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Ното

Synthetic.

The present invention describes a composition which comprises a therapeutic agent that reduces the amount of active heat shock protein 27 (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising a therapeutic agent that reduces the amount of active hsp27 in hsp27 expressing cells exposed to the therapeutic agent, useful in treating cancer, e.g., prostate cancer or a central nervous
 composition has cytostatic activity, and can be used in gene therapy. The
            composition is useful in treating cancer, e.g., prostate, bladder, lung, breast, pancreatic, colon, skin (for example melanoma), renal or ovarian cancer or a central nervous system malignancy. The present sequence represents a human hap27 antisense oligonucleotide which is used in the exemplification of the present invention.
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heat shock protein 27; hsp27; cytostatic; gene therapy;
heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
                                                                                                                                                                                             ;
                                                                                                                                                         Score 20; DB 12; Length 20;
Pred. No. 12;
                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signaevsky M;
                                                                                                                                                                                                                              1 GGGACGCGCGCTCGGTCAT 20
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                                                                                                                                                       Query Match

Best Local Similarity 100.0%;

Matches 20; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2002; 2002US-0415859P.
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                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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system malignancy
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ADM94731
ID ADM9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            composition comprising a therapeutic agent that reduces the amount of ive hsp27 in hsp27 expressing cells exposed to the therapeutic agent, ful in treating cancer, e.g., prostate cancer or a central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                       heat shock protein 27; hsp27; cytostatic; gene therapy;
heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
short interfering RNA; siRNA; RNA interference; RNAi; ds.
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                                                                                                                                                                                              Human heat shock protein 27 siRNA oligonucleotide SEQ ID NO:90.
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100.0%; Pred. No. ---
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               GGGACGCGCGCTCGGTCAT 21
1 GGGACGCGCGCTCGGTCAT 20
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18-APR-2003; 2003US-0463952P.
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                                                                                                       ADM94740 standard; DNA; 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system malignancy.
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                                                                          RESULT 3
ADM94740/c
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Gaps

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Query Match 100.0%; Score 20; DB 12; Length 21; Best Local Similarity 100.0%; Pred. No. 12; Matches 20; Conservative 0; Mismatches 0; Indels

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New composition comprising a therapeutic agent that reduces the amount of active hep21 in hsp27 expressing cells exposed to the therapeutic agent, useful in treating cancer, e.g., prostate cancer or a central nervous system malignancy.
                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a composition which comprises a therapeutic agent that reduces the amount of active heat shock protein 27 (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The composition has cytostatic activity, and can be used in gene therapy. The composition is useful in treating cancer, e.g., prostate, bladder, lung, breast, pancreatic, colon, skin (for example melanoma), renal or ovarian cancer or a central nervous system malignancy. The present sequence represents a human hsp27 antisense oligonucleotide which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; pASK-MBD; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic product 2 reverse PCR primer for construction of pASK-MBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15; DB 12; Length 21;
Pred. No. 2.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 4 A; 5 C; 11 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                    Signaevsky
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                                                                                                        (UYBR-) UNIV BRITISH COLUMBIA
    02-OCT-2003; 2003WO-CA001588
                                          02-OCT-2002; 2002US-0415859P.
18-APR-2003; 2003US-0463952P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 GGGACGCGCGCTCG
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                                                                                                                                                  Rocchi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-435437/46.
                                                                                                                                                                                          WPI; 2004-316331/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Summers AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-2002.
                                                                                                                                                  Gleave ME,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK52211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a composition which comprises a therapeutic agent that reduces the amount of active heat shock protein 27 (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The composition has cytostatic activity, and can be used in gene therapy. The composition is useful in treating cancer, e.g., prostate, bladder, lung, breast, pancreatic, colon, skin (for example melanoma), renal or ovarian cancer or a central nervous system malignancy. The present sequence represents a human hsp27 antisense oligonucleotide which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising a therapeutic agent that reduces the amount of active hsp27 in hsp27 expressing cells exposed to the therapeutic agent, useful in treating cancer, e.g., prostate cancer or a central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:4.
Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:3
                                        heat shock protein 27; hsp27; cytostatic; gene therapy;
heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heat shock protein 27; hsp27; cytostatic; gene therapy; heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human; antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 16; DB 12; Length 21; 100.0%; Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 1 A; 7 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               Signaevsky M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 3; 38pp; English
                                                                                  antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM94654 standard; DNA; 21 BP.
                                                                                                                                                                                                                                                                          02-OCT-2003; 2003WO-CA001588.
                                                                                                                                                                                                                                                                                                                  02-OCT-2002; 2002US-0415859P
18-APR-2003; 2003US-0463952P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 CGCGCCGCTCGGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                           Rocchi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-316331/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                system malignancy.
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                                                                                                                                                                                      WO2004030660-A2
                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Gleave ME,

15-APR-2004

Synthetic

01-JUL-2004

ADM94654;

Query Match

Best Loc Matches

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15-APR-2004

Synthetic

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Gaps

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The present invention relates to a new non-naturally occurring

recombinant DNA molecule comprising a sequence encoding a chelon protein

which bluds mercuric ions. The invention is useful for recombinantly

producing a protein in a host-cell, by infecting or transforming host

cell capable of expressing a chelon coding sequence with a vector

cell capable of expressing a chelon coding sequence with a vector

cell capable of expressing a chelon coding sequence with a vector

cell capable of expressing a chelon protein is useful for binding divalent

region for the protein to produce a recombinant host cell and culturing

the recombinant host cell under conditions, where DNA is expressed. The

mucleic acid encoding the chelon protein is useful for binding divalent

mercuric ions, to take up, sequester and concentrate the heavy metal ions

from contaminated soil, ground water, hydroponic solutions or irrigation

water of waste streams. The DNA of the invention, when immobilised onto a

contaminated environment waste streams or contaminated aqueous medium

contaminated ions such as mercury and/or cadmium. The molecules of the

contaminated ions such as mercury and/or cadmium. The molecules of the

contaminated ions such as mercury and/or cadmium. The molecules of the

contaminated invention is highly specific and binds divalent cation such as

mercury or cadmium with high affinity. The present nucleic acid sequence

represents synthetic product 2 reverse PCR primer that was used in the

contaminated advalent product 2 reverse PCR primer that was used in the

contaminated and morphaled and the present molecules and the processed to the invention as a synthetic produc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene expression analysis; array; hybridisation; genetic variation; tag-labelled compound; gene family; in situ hybridisation; library screening; Southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection; target sequence; probe; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA target sequence #7242 useful in array for genetic analyses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 71.0%; Score 14.2; DB 6; Length 33; Local Similarity 84.2%; Pred. No. 5.48+03; les 16; Conservative 0; Mismatches 3: ThARA
soil, water, aqueous medium including biological fluids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33 BP; 6 A; 8 C; 12 G; 7 T; 0 U; 0 Other;
                                               Disclosure; Page 24; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGGACGCGCCCTCGGTCA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GGGTCTCGGCGCTCGGGCA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACH58106 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-2002; 2002US-00215112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-AUG-2001; 2001US-0311040P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-576608/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MITT/) MITTMANN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003082596-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACH58106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, antisense match or antisense mismatch oligonucleotides. The probes may be used in an array is useful in monitoring gene expression nucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic variations, and in hybridisations in screening cDNA or genomic libraries useful for identifying family members of a gene. The probes are useful in in situ hybridisations, in screening cDNA or genomic libraries (or derived subclones) for additional clones containing segments of DNA that have been previously isolated and sequenced, in Southern, northern, or dot-blot hybridisation of genomic DNA to identify or detect the sequence of any gene or detect specific mutations in any gene, and in mapping the 5' termini of mand locules by primer extensions. The nucleic acid sequences of the invention are also useful as PCR primers. The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical uses. ARHSO865-ACH65260 represent the target sequences of the invention. Note: The sequence data for this patent was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
analyzing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.0%; Score 14; DB 9; Length 25; 100.0%; Pred. No. 6.8e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human microarray DNA oligonucleotide SEQ ID NO 3853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 BP; 4 A; 9 C; 9 G; 3 T; 0 U; 0 Other;
                                                              Claim 1; SEQ ID NO 7242; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACI03862 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGACGCGCCCTCG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGACGCGCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003104410-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mittmann MP;
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ACI03862/c
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The Inventors a mathematical approach as the problem in the inventors of t invention discloses a microarray comprising a plurality of nucleic Sequence 25 BP; 6 A; 8 C; 8 G; 3 T; 0 U; 0 Other; from USPTO at segdata.uspto.goc/sequence.html SEQ ID NO 3853; 9pp; English. Claim 1; 

Query Match 66.0%; Score 13.2; DB 9; Length 25; Best Local Similarity 83.3%; Pred. No. 1.6e+04; Matches 15; Conservative 0; Mismatches 3; Indels 2 GGACGCGCGCTCGGTCA 19 -24 ddacregredered g ð

ACI65798 standard; DNA; 25 BP. 14-0CT-2003 ACI65798; RESULT 9 ACI 65798 

Human microarray DNA oligonucleotide SEQ ID NO 65789. (first entry)

expression; EST; ss; probe; expressed sequence tag; microarray; gene genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

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US2003104410-A1.

05-JUN-2003

15-MAR-2002; 2002US-00098263

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC.

Mittmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 65789; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises comparises and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the concleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific.

Cut family members of a gene and a cross-species comparison.

Cut family members of a gene and a cross-species comparison.

Cut family members of a gene and a cross-species comparison.

Cut family members of a gene and a cross-species comparison.

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Cut family members of a gene and a cross-species comparison.

Cut family members of a gene and a cross-species comparison.

Cut family members of a gene of the microarray. Note: The sequence of the comparison of the comparison of the comparison of the comparison of the from USPTO at segdata.uspto.goc/sequence.html 

Sequence 25 BP; 4 A; 8 C; 9 G; 4 T; 0 U; 0 Other;

Gaps ; Length 25; 3; Indels Score 13.2; DB 9; Pred. No. 1.6e+04; Mismatches ö 66.0%; 83.3%; Query Match
Best Local Similarity 83.5%,
Local Similarity 83.5%,
Local Similarity

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GACGCGCGCTCGGTCAT 20 GACCCGGAGCTCGGTCGT 22 m

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Gaps

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RESULT 10 AAH21740

BP. AAH21740 standard; DNA; 27 14-AUG-2001 (first entry) AAH21740; 

Corynebacterium glutamicum chaperone CpkB related PCR primer SEQ:13.

Corynebacterium glutamicum; chaperone; chaperonin; CpkB; groEL; fermentation; L-glutamic acid; thermophilic microbe; PCR primer; ss. Corynebacterium glutamicum

JP2001069979-A.

21-MAR-2001.

99JP-00245121. 31-AUG-1999; 99JP-00245121 31-AUG-1999;

(NISB ) JAPAN TOBACCO INC. (BEAB-) BE ABLE KK.

WPI; 2001-321175/34.

Preparation of L-glutamic acid by fermentation.

Example 1; Page 11; 18pp; Japanese.

The present invention describes an L-glutamic acid-producing microbe (I) to its mutant which expresses the molecular chaperone derived from a thermophilic microbe and produces stably L-glutamic acid at a temperature near the upper limit of optimum growth or higher. (I) or its mutant transformed by a recombinant DNA containing a gene encoding the molecular

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chaperone derived from a thermophilic microbe and a promoter operably associated with a gene (II) comprising: (a) a fully defined 1661 base pair (bp) sequence (AAH21157); (b) a nucleic acid sequence encoding a protein comprising: (i) a base sequence in which 1-20 bases are deleted, replaced or added in AAH21757; or (ii) at least one base is deleted, replaced or added in a fully defined 519 base sequence (AAH21768), and having molecular chaperone activity in (I). Also described is a method for the preparation of L-glutamic acid by fermentation in which the production of L-glutamic acid with the untransformed (I) is used and cultured at a high temperature limiting the production of L-glutamic acid with the untransformed (I). The microbe can be used for the preparation of L-glutamic acid. The present sequence represents a PCR primer used in the preparation of Corynebacterium glutamicum chaperone CpkB, which is used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV51401-V51704 are forward PCR primers used to amplify fragments of the Zea mays genome in order to detect polymorphic markers. Such markers can be used in the construction of allele-specific primers and probes for amplification or hybridisation, e.g. to determine common or disparate ancestry between 2 or more plants, to monitor the genetic contribution of an ancestral plant, to trace the progeny of proprietary plants, in certification of a hybrid plant or to identify the progeny of a back-crossed plant with an ancestral plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphic marker; allele-specific; probe; amplification; PCR primer; hybridisation; plant; hybrid certification; genetic contribution; progeny; back-cross; hybrid; ancestry; corn; ss.
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     species allele-specific oligonucleotide probes and primers
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0
                                                                                                                                                                                                                                                                                                                        66.0%; Score 13.2; DB 4; Length 27; 83.3%; Pred. No. 1.6e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murigneux A;
                                                                                                                                                                                                                                                                                    Sequence 27 BP; 4 A; 9 C; 8 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays genome forward PCR primer #304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sapolsky RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 55; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
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97US-00813507
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                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 3 GACGCGCCCTCGGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                  9 gacgcggcgaacggccar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV51704 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Landry BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-333252/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9824796-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-FEB-1999
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                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV51704;
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                                                                                                                                                                                                                                                                                                                          Query Match
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Sequence 21 BP; 3 A; 11 C; 4 G; 3 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid sequences that hybridize to the pBR322 origin of replication, useful for monitoring gene therapy vectors, and as probes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA75311-41 and AAA75393-A75402 are derived from the origin of replication of the pBR322 plasmid. The nucleic acid fragments are useful as probes and primers for detecting sequences derived from the origin of replication of pBR322 or vectors (or their fragments) that contain such sequences. They are particularly used to monitor the presence of gene therapy vectors (used to deliver therapeutic genes or proteins, antisense sequences or ribozymes), e.g. for determining disappearance of the vector, for adjustment of treatment, or for timing of new treatments. They can also be used to screen foods and cosmetics for the presence of
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
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   Length 21;
                                                                                                                                                                                                                                                   Pragment derived from the origin of replication of pBR322.
                               Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              derived materials from genetically modified organisms
                                                                                                                                                                                                                                                                              probe; primer; origin of replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 6 A; 7 C; 8 G; 2 T; 0 U; 0 Other;
                              7
Score 12.8; DB 2;
Pred. No. 2.4e+04;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.0%; Score 12.8; DB 3;
87.5%; Pred. No. 2.4e+04;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 26; 36pp; French.
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 Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABZ58873 standard; DNA; 24
                                                                                                                                                             AAA75395 standard; DNA; 23
                                                                                                                                                                                                                     15-JAN-2001 (first entry)
                                                                                       16 GGGACGAGGCGCTGGG
                                                           GGGACGCGCGCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.5'
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cecrececrecerear
                                                                                                                                                                                                                                                                                            gene therapy vector; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-587445/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TRGE ) TRANSGENE
                                                                                                                                                                                                                                                                             pBR322 plasmid;
                                                                                                                                                                                                                                                                                                                                                    WO200053803-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000,
                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                          AAA75395;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primers
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ABZ58873
ID ABZ58:
XX
AC ABZ58:
XX
                                                                                                                                  RESULT 12
                                                                                                                                               AAA75395,
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

C perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, or analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridisation at least one or more nucleic acids to at least two or more nucleic acids to at least two or more concept analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms.

C probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms.

C ramily members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific with any gene, in mapping the 5' terminin of marken sor subcilies or subcilies or any gene, in mapping the 5' terminin of marken sor subcilies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.obtained in electronic format directly
                                                                                                                                                                                                                                                                                                         New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, CFTR gene, 88; probe, cystic fibrosis;
Oystic Fibrosis Transmembrane Conductance Regulator;
invasive cleavage structure assay; INVADER, FRET;
fluorescent resonance energy transfer; multiplexed amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.0%; Score 12.8; DB 9; Length 25; 87.5%; Pred. No. 2.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CFTR gene wild-type probe for variant S549N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 BP; 4 A; 9 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 84528; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                      16-MAR-2001; 2001US-0276759P.
                                  15-MAR-2002; 2002US-00098263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGACGCGCGCTCGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 GGGACACGGCACTCGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADO31537 Btandard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
                                                                                                                                          (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                     WPI; 2003-567953/53.
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                                                                                                                                                                                                 Mittmann MP;
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ADO31537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a teleost (zebrafish) ERG (ZERG) polypeptide. The ZERG nucleic acid molecule is useful for studying cardiac function, abnormal heart beat phenotype, or long QT syndrome (an abnormality of cardiac muscle repolarization that predisposes affected individuals to lethal arrhythmias). The zebrafish comprising ZERG genes are particularly useful for cardiac function or disease. The ZERG genes are particularly useful for in (non-) cardiac researches, or for developing treatments for cardiac diseases, tumours or cancers, brain and nervous system disorders sequence represents the zebrafish ZERG mRNA inhibiting antisense oligonucleotide. (Updated on 27-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New teleost (specifically zebrafish) ERG genes, which encode ERG family potassium channels, useful for studying e.g. cardiac or brain function, or for developing treatments for e.g. cardiac diseases, cancer or neurological diseases.
                                                                                                                                    Teleost; zebrafish; ZERG; cardiovascular; antiarrhythmic; cytostatic; neuroprotective; gene therapy; potassium channel; antisense; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
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                                                                           Zebrafish ZERG mRNA inhibiting antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human microarray DNA oligonucleotide SEQ ID NO 84528.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 28; 55pp; English.
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ACI84537 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                       11-JUL-2002; 2002WO-IB004280.
                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUL-2001; 2001US-0305396P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCGGCGCACGGGCAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 CGCGGCGCTCGGTCAT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ARTE-) ARTEMIS PHARM GMBH
                            (first entry)
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(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-210421/20.
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Best Local Similarity
                                                                                                                                                                                                                                                                         WO2003006502-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Langheinrich U;
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27-OCT-2003
28-APR-2003
                                                                                                                                                                                                                     Danio rerio.
                                                                                                                                                                                                                                                                                                                                23-JAN-2003
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Matches

RESULT 14 ACI84537

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Gaps

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2; Indels

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The invention relates to detecting Cystic Fibrosis Transmembrane
Conductance Regulator (CFTR) alleles comprising providing a sample
Comprising a CFTR target nucleic acid, amplifying the CFTR target nucleic
acid with 25 cycles or fewer of a PCR to generate amplified target nucleic
conditions such that the acid, and exposing the amplified target nucleic acid, and exposing the amplified target nucleic acid, and exposing the amplified target nucleic acid to detection
consensor resonance energy transfer). Also included is a kit
cleavage structure assay (designated INVADER), employing FRET probes
CC (fluorescent resonance energy transfer). Also included is a kit
comprising at least one CFTR allele or oligonucleotide detection assays
CC comprising the configured for detecting a set of CFTR alleles where the set is a first
configured for detecting a set of CFTR alleles where the set is a first
configured for detecting a set of CFTR alleles where the set is a first
configured for detecting a set of CFTR alleles where the set is a first
configured for detecting a set of CFTR alleles to a third set
configured for the comprising 310+1G to A, dells 0,
CC 1148T, and A455E, a second set comprising 310+1G to A, 3659delC, G551D,
CC 01190nucleotide configured to form an invasive cleavage structure in
comprising R347P, G35E, G542X and R553X, or a fifth set comprising
CC oligonucleotide detection assays comprises first and second
coligonucleotide comprises a 5' portion and a 3' portion, where the 3'
CC onbination with a target sequence comprising the CFTR allele. The first
coligonucleotide comprises a 5' portion and a 3' portion, where the 5'
CC portion is configured to hybridise to the target sequence and the 3'
CC portion is configured to hybridise to the target sequence and the 3'
CC portion is configured to hybridise to the target sequence and the 3'
CC portion is configured to hybridise to the target sequence and the solution and with are useful for a partion and the solution and kit are useful for a partion and the solution 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) alleles, useful for screening mutations associated with cystic fibrosis, comprises exposing amplified CFTR target nucleic acid to detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and kit are useful for detecting CFTR alleles, more particularly for screening nucleic acid samples e.g. from patients, for the presence of any one of a collection of mutations in the CFTR gene associated with cystic fibrosis. The method and compositions are useful for generating and analysing limited cycle, multiplexed amplification of a large collection of CFTR loci. The present sequence comprises a probe for the method of the invention detecting the wild-type CFTR allele.
                                                                                                                                                                                                                                                                                                                            , Bartholomay CT, Kwiatkowski RW;
Peterson P, Agarwal P, Jarvis N;
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"S. Carroll K, I
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26-JUN-2003; 2003US-00606577.
21-JUL-2003; 2003US-0489055P.
25-AUG-2003; 2003US-0497644P.
28-OCT-2003; 2003US-0515175P.
14-NOV-2003; 2003US-00713653.
14-NOV-2003; 2003WO-US036611
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                                                       14-NOV-2002;
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Hall JG,
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Search completed: May 8, 2006, 09:17:44 Job time : 281 secs

3 GGACGCGGAGCTCAGT 18

2 GGACGCGCGCTCGGT 17

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Sequence 90, Appl
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Sequence 405955,
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Sequence 81, Appl
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| SIDSS/ptodata/2/pubpna/USOB_NEW_PUB.seq1:*
| SIDSS/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
| SIDSS/ptodata/2/pubpna/USOB_NEW_PUB.seq:**
GenCore version 5.1.8
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US-10-310-914A-1230089
US-10-310-914A-194776
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C 20 13.8 69.0 25 17 US-11-121-649-405692 C 21 13.6 68.0 21 10 US-10-10-914A-1271039 C 22 13.6 68.0 21 10 US-10-10-914A-1271039 C 22 13.6 68.0 21 10 US-10-110-914A-1271039 C 24 13.4 67.0 12 10 US-10-110-914A-62775 C 24 13.4 67.0 22 18 US-11-128-665-70 19 US-10-110-914A-868771 C 25 13.4 67.0 22 18 US-11-148-423-82 C 27 13.4 67.0 22 18 US-11-148-423-82 C 27 13.4 67.0 22 18 US-11-148-4133 3 13.2 66.0 19 10 US-10-10-914A-62775 C 29 13.2 66.0 19 10 US-10-10-914A-62712 C 29 13.2 66.0 19 10 US-10-10-914A-62925 C 34 13.2 66.0 25 17 US-11-121-849-14312 C 35 13 13.2 66.0 25 17 US-11-121-849-14312 C 35 13 13.2 66.0 25 17 US-11-121-849-14312 C 35 17 US-11-130-914A-6072 C 41 12.8 64.0 19 10 US-10-934-964211 C 42 12.8 64.0 19 10 US-10-914A-6074 C 44 12.8 64.0 19 10 US-10-914A-6074 C 44 12.8 64.0 19 10 US-10-910-914A-6074 C 44 12.8 64.0 19 10 US-10-910-914A-6074 C 44 12.8 64.0 19 10 US-10-910-914A-26494 C 45 12.8 64.0 19 10 US-10-910-914A-914A-914 C 45 12.8 64.0 19 10 US-10-910-914A-914 C 45 12.8 64.0 19 10 US-10-910-914A-914 C 45 12.8 64.0 19 10 US-10-910-914A-914 C 45 12.8 64.0 19 10 US-10-910-914 C	US-10-932-182A-16224	Sequence	16224,
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C 22 13.6 68.0 21 10 US-10-10-914A-371039 C 23 13.4 67.0 19 10 US-10-110-914A-271039 C 24 13.5 68.0 21 10 US-10-110-914A-271039 C 25 13.4 67.0 22 18 US-11-18-423-86 C 27 13.4 67.0 22 18 US-11-18-423-86 C 27 13.4 67.0 26 10 US-10-110-914A-1239636 C 27 13.4 67.0 26 10 US-10-110-914A-41239636 C 28 13.2 66.0 19 10 US-10-10-914A-41333 29 13.2 66.0 19 10 US-10-10-914A-41333 21 13.2 66.0 19 10 US-10-10-914A-41333 21 13.2 66.0 21 10 US-10-914A-612113 21 13.2 66.0 22 11 US-10-914A-612112 23 13.2 66.0 25 11 US-10-914A-61212 C 34 13.2 66.0 25 11 US-10-914A-61212 C 35 13 65.0 25 11 US-10-914A-60726 C 41 12 64.0 19 10 US-10-10-914A-60726 C 41 12.8 64.0 19 10 US-10-110-914A-60726 C 5 17 US-10-110-914A-721661 C 6 1 18 US-10-110-914A-60726 C 7 1 US-10-10-914A-721661 C 7 1 US-10-10-914A-721661 C 8 1 US-10-110-914A-721661 C 9 1 US-10-110-914A-721661 C 1 US-10-110-914A-984231 C 1 US-10-10-914A-984231 C 1 US-10-10-914A-914A-914A-914A-91	US-11-121-849-405692	Seguence	405692,
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25 13.4 67.0 20 10 US-10-1148-42-82-82  26 26 13.4 67.0 26 10 US-10-310-9144-2887/1  27 13.4 67.0 26 10 US-10-310-9144-2883/3  28 13.2 66.0 18 10 US-10-310-9144-41833  29 13.2 66.0 19 10 US-10-310-9144-41833  30 13.2 66.0 21 10 US-10-310-9144-41833  31 13.2 66.0 24 10 US-10-310-9144-41833  32 13.2 66.0 24 10 US-10-310-9144-615113  31 13.2 66.0 25 17 US-11-12-849-39056  33 13.2 66.0 25 17 US-11-13-849-39056  34 13.2 66.0 25 17 US-11-13-87-20146  35 13.2 66.0 25 17 US-11-13-67-20146  36 13 65.0 25 11 US-10-934-867/26  41 12.8 64.0 19 10 US-10-934-667/27  42 12.8 64.0 19 10 US-10-9144-607/27  43 12.8 64.0 19 10 US-10-9144-607/27  44 12.8 64.0 19 10 US-10-9144-607/27  45 12.8 64.0 19 10 US-10-9144-607/27  47 12.8 64.0 19 10 US-10-9144-607/27  48 64.0 19 10 US-10-9144-607/27  49 12.8 64.0 19 10 US-10-9144-607/27  40 12.8 64.0 19 10 US-10-9144-607/27  41 12.8 64.0 19 10 US-10-9144-607/27  42 12.8 64.0 19 10 US-10-9144-607/27  43 12.8 64.0 19 10 US-10-9144-607/27  44 12.8 64.0 19 10 US-10-91-944-607/27  5 SQUARENT ROCCHI, Palma APPLICANT: ROCCHI, Palma APPLICANT	US-10-310-914A-625756	Sequence	625756,
25 13.4 67.0 22 18 US-11-1310-3148-123-8  2 2 13.4 67.0 22 18 US-11-1310-3144-1832  2 2 13.4 67.0 20 10 US-10-310-9144-1833  2 13.2 66.0 19 10 US-10-310-9144-41833  3 13.2 66.0 21 10 US-10-314-41833  3 13.2 66.0 21 10 US-10-314-41833  3 13.2 66.0 21 10 US-10-314-48-59926  3 3 13.2 66.0 25 17 US-10-9144-659926  3 3 13.2 66.0 25 17 US-10-9144-639926  3 3 13.2 66.0 25 17 US-10-9144-639926  3 3 13.2 66.0 25 17 US-10-9144-67916  5 3 13.2 66.0 25 17 US-10-934-982-151912  5 4 13.2 8 64.0 19 10 US-10-9144-67944  5 5 12.8 64.0 19 10 US-10-9144-67944  5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	US-10-310-914A-968771	Sequence	968771,
C 25 13.4 67.0 36 10 US-10-314-123636 C 28 13.4 67.0 36 10 US-10-310-914A-1239636 C 28 13.2 66.0 19 10 US-10-310-914A-1833 30 13.2 66.0 19 10 US-10-310-914A-1833 30 13.2 66.0 24 10 US-10-310-914A-65312 31 13.2 66.0 24 10 US-10-310-914A-65312 32 13.2 66.0 25 17 US-10-914A-63926 33 13.2 66.0 25 17 US-10-914A-63926 25 13 US-10-933-982-120239 25 13 2 66.0 25 17 US-11-136-827-29166 C 36 13.2 66.0 25 17 US-11-136-827-29166 C 36 13.2 66.0 25 17 US-10-933-982-120239 25 13 65.0 25 11 US-10-934-984-60727 C 44 12.8 64.0 19 10 US-10-934-984-60727 C 42 12.8 64.0 19 10 US-10-934-984-261943 C 43 12.8 64.0 19 10 US-10-310-914A-60727 C 43 12.8 64.0 19 10 US-10-310-914A	US-11-148-423-82	Sequence	82, Appl
C 27 13.4 67.0 30 14 US-11-226-607-70  C 27 13.2 66.0 18 10 US-10-310-914A-130393  29 13.2 66.0 19 10 US-10-310-914A-65912  31 13.2 66.0 24 10 US-10-310-914A-65912  32 13.2 66.0 25 10 US-10-310-914A-65912  33 13.2 66.0 25 10 US-10-310-914A-639926  34 13.2 66.0 25 17 US-11-121-849-39050  C 35 17 US-11-121-849-39050  C 36 13 65.0 25 11 US-10-934-867-1150  C 40 12.8 64.0 19 10 US-10-914A-607-2  C 41 12.8 64.0 19 10 US-10-914A-607-2  C 42 12.8 64.0 19 10 US-10-914A-607-4  C 42 12.8 64.0 19 10 US-10-914A-607-4  C 43 12.8 64.0 19 10 US-10-914A-607-4  C 44 12.8 64.0 19 10 US-10-914A-607-4  C 45 12.8 64.0 19 10 US-10-914A-984231  ALIGNMENTS  RESULT 1  APPLICANT: SIGNESHION NUMBER: US/11/262,388  CURRENT FILING DATE: 2005-10-02  PRIOR APLICATION NUMBER: US/11/262,388  CURRENT FILING DATE: 2005-10-02  PRIOR APLICATION NUMBER: US/10/605,498  PRIOR FILING DATE: 2005-10-02  PRIOR APLICATION NUMBER: US/10/605,498  PRIOR FILING DATE: 2003-10-02  PRIOR PRIOR PRIUGATION NUMBER: US/10/605,498  PRIOR FILING DATE: 2003-10-02  PRIOR PRIOR FILING DATE: 2003-10-03  SSEQ ID NO SEED ID	US-10-310-914A-1239636	Sequence	1239636,
C 28 13.2 66.0 18 10 US-10-310-914A-41833 3 13.2 66.0 19 10 US-10-310-914A-41833 3 13.2 66.0 21 10 US-10-310-914A-61513 31 13.2 66.0 22 10 US-10-310-914A-61513 31 13.2 66.0 25 17 US-11-121-849-19050 33 13.2 66.0 25 17 US-11-121-849-19050 34 13.2 66.0 25 17 US-11-121-849-19050 53 13.2 66.0 25 17 US-11-121-849-19050 54 13.2 66.0 25 11 US-10-934-60727 55 13 65.0 25 11 US-10-934-60727 56 13 65.0 25 11 US-10-934-60727 57 12.8 64.0 18 10 US-10-934-60727 58 64.0 19 10 US-10-934-60727 59 12.8 64.0 19 10 US-10-914A-60727 59 12.8 64.0 19 10 US-10-914A-60727 50 12.8 64.0 19 10 US-10-914A-984231 50 10 12 12 12 12 12 12 12 12 12 12 12 12 12	US-11-226-605-70	Seguence	70, Appl
29 13.2 66.0 19 10 US-10-314A-41833 30 13.2 66.0 21 10 US-10-310-914A-41833 31 13.2 66.0 24 10 US-10-310-914A-629113 31 13.2 66.0 25 10 US-10-310-914A-629126 33 13.2 66.0 25 17 US-11-121-849-19050  C 34 13.2 66.0 25 17 US-11-121-849-143212 35 13.2 66.0 25 17 US-11-121-849-143212 37 13.6 5.0 25 11 US-10-933-982-120239 37 13 65.0 25 11 US-10-933-982-151912 38 13 65.0 25 11 US-10-914A-60726 C 40 12.8 64.0 18 10 US-10-914A-60726 C 41 12.8 64.0 19 10 US-10-914A-60724 C 42 12.8 64.0 19 10 US-10-914A-60744 C 43 12.8 64.0 19 10 US-10-914A-60744 C 44 12.8 64.0 19 10 US-10-914A-984231 C 45 12.8 64.0 19 10 US-10-914A-60744 C 45 12.8 64.0 19 10 US-10-914A-60744 C 45 12.8 64.0 19 10 US-10-914A-60744 C 45 12.8 64.0 19 10 US-10-914A-984231 C 45 12.8 64.0 19 10 US-10-910-914A-984231 C 45 12.8 64.0 10 US-10-910-914A-984231 C 45 12.8 64.0 10 US-10-910-914A-984231 C 45 12.8 64.0 10 US-10-910-910-910-910-910-910-910-910-910-	US-10-310-914A-1303083	Sequence	1303083,
30 13.2 66.0 21 10 US-10-310-914A-615113 31 13.2 66.0 24 10 US-10-310-914A-615113 31 13.2 66.0 25 10 US-10-310-914A-61512 33 13.2 66.0 25 17 US-11-121-849-13050 c 34 13.2 66.0 25 17 US-11-121-849-13050 c 35 13.2 66.0 25 17 US-11-121-849-13050 c 36 13.2 66.0 25 17 US-11-121-849-13012 37 13 65.0 25 11 US-10-933-982-151912 39 13 65.0 25 11 US-10-933-982-151912 c 38 13 65.0 25 11 US-10-933-982-151912 c 40 12.8 64.0 18 10 US-10-914A-72166 c 41 12.8 64.0 19 10 US-10-914A-60724 c 42 12.8 64.0 19 10 US-10-914A-60724 c 43 12.8 64.0 19 10 US-10-914A-60724 c 44 12.8 64.0 19 10 US-10-914A-60727 c 45 12.8 64.0 19 10 US-10-914A-60727 c 45 12.8 64.0 19 10 US-10-914A-60727 c 47 12.8 64.0 19 10 US-10-914A-60727 c 48 12.8 64.0 19 10 US-10-914A-60727 c 49 12.8 64.0 19 10 US-10-914A-60727 c 47 12.8 64.0 19 10 US-10-914A-60727 c 48 12.8 64.0 19 10 US-10-914A-60727 c 49 12.8 64.0 19 10 US-10-914A-60727 c 7 12.8 64.0 19 10 US-10-914A-60727 c 48 12.8 64.0 19 10 US-10-914A-60727 c 49 12.8 64.0 19 10 US-10-310-914A-7818 c BENERAL INFORMATION: c APPLICANT: Gleave, Martin APPLICANT: Gleave, Mart	US-10-310-914A-41833	Sequence	41833, A
31 13.2 66.0 24 10 US-10-310-914A-62912 32 13.2 66.0 25 10 US-10-310-914A-62912 33 13.2 66.0 25 17 US-11-121-849-39050 c 34 13.2 66.0 25 17 US-11-121-849-39050 c 35 13 2 66.0 25 17 US-11-121-849-39050 c 36 13 65.0 25 17 US-11-136-527-297166 c 36 13 65.0 25 11 US-10-933-982-120239 c 38 13 65.0 25 11 US-10-933-982-120239 c 39 13 65.0 25 11 US-10-933-982-201040 39 13 65.0 25 11 US-10-933-982-201040 39 13 65.0 25 11 US-10-934-048A-115670 c 40 12.8 64.0 18 10 US-10-914A-60726 c 41 12.8 64.0 19 10 US-10-914A-60727 c 42 12.8 64.0 19 10 US-10-914A-61343 c 45 12.8 64.0 19 10 US-10-914A-984231 c APPLICANT: Gleave, Martin APPLICANT: Rocchi, Palm TITLE OF INVENTION: Compositions and Methods for Treatmen TITLE OF INVENTION: Compositions and Methods for Treatmen FILE REFERENCE: UGC-031 CURRENT APPLICATION NUMBER: US/11/262,388 PRIOR FILING DATE: 2003-10-02 PRIOR PILING DATE: 2003-10-02 PRIOR FILING DATE: 2003-10-02 PRIOR FILING DATE: 2003-04-18 NUMBER OF SEQ ID NOS: 91 PRIOR FILING DATE: 2003-04-18 NUMBER OF SEQ ID NOS: 91 LENGTH: 2003-04-18 SEQ ID NOS: 91 LENGTH: 2003-04-18 LENGTH: 2003-04-18	US-10-310-914A-615113	Sequence	615113,
13. 13.2 66.0 25 10 US-10-110-914A-83926 33 13.2 66.0 25 17 US-11-121-849-39050 24 13.2 66.0 25 17 US-11-121-849-143212 35 13.2 66.0 25 17 US-11-121-849-143212 36.0 25 17 US-11-121-849-14321 27 13.2 66.0 25 17 US-11-121-849-143212 27 13 65.0 25 11 US-10-933-982-151912 27 23 13 65.0 25 11 US-10-933-982-151912 27 23 13 65.0 25 11 US-10-933-982-151912 27 24 12.8 64.0 12 18 10 US-10-110-914A-60726 24 12.8 64.0 19 10 US-10-310-914A-60727 24 12.8 64.0 19 10 US-10-310-914A-60744 27 24 12.8 64.0 19 10 US-10-310-914A-60744 27 24 12.8 64.0 19 10 US-10-310-914A-60744 27 24 12.8 64.0 19 10 US-10-310-914A-984231 28 209-10-28 22 2000040866A1 28 2.0 200040866A1 28 20004086A1 28 20004086A1 28 200040866A1 28 20004086A1 28 20004086A1 28 20004086A1 28 20004086A1 28 200040886A1 28 200040886A1 28 200040886A1 28 200040886A1 28 200040886A1 28 200040886A1 28 20004088 20 20004088 20 20 20 20 20 20 20 20 20 20 20 20 20	US-10-310-914A-62912	Sequence	62912, A
2 3 13.2 66.0 25 17 US-11-121-849-39050 2 3 4 13.2 66.0 25 17 US-11-121-849-13212 3 5 13.2 66.0 25 17 US-11-121-849-13212 2 3 6 13.2 66.0 25 17 US-11-121-849-120239 2 3 13.5 65.0 25 11 US-10-933-982-151912 2 3 8 13 65.0 25 11 US-10-933-982-151912 2 3 9 13 65.0 25 11 US-10-933-982-151912 3 9 13 65.0 25 11 US-10-914A-721661 2 40 12.8 64.0 19 10 US-10-914A-721661 2 42 12.8 64.0 19 10 US-10-914A-721691 2 44 12.8 64.0 19 10 US-10-914A-261943 2 45 12.8 64.0 19 10 US-10-914A-261943 2 45 12.8 64.0 19 10 US-10-914A-984231 3 SEQUENCE 82, Martin 3 APPLICANT: Signaevsky, Maxim 4 TITLE 0F INVENTION: Compositions and Methods for Treatmen; 5 TILE DEPERBNCE: UBC.P-031 5 TILE DEPERBNCE: UBC.P-031 5 TILE DEPERBNCE: UBC.P-031 5 TILE DEPERBNCE: UBC.P-031 5 PRIOR APPLICATION NUMBER: US 60/415,859 5 PRIOR FILING DATE: 2002-10-02 5 PRIOR FILING DATE: 2002-10-02 5 PRIOR FILING DATE: 2002-10-02 5 PRIOR FILING DATE: 2003-04-18 5 NUMBER OF SEQ ID NOS: 91 5 SEQ UBNOS: 91	US-10-310-914A-839926	Sequence	839926,
c 34 13.2 66.0 25 17 US-11-121-849-143312  c 36 13.2 66.0 25 17 US-11-121-849-143312  c 36 13.2 66.0 25 17 US-11-136-527-297166  3 13 65.0 25 11 US-10-933-982-151912  c 38 13 65.0 25 11 US-10-933-982-151912  c 40 12.8 64.0 18 10 US-10-914A-60726  c 41 12.8 64.0 18 10 US-10-914A-60747  c 43 12.8 64.0 19 10 US-10-914A-60747  c 44 12.8 64.0 19 10 US-10-914A-984231  c 45 12.8 64.0 19 10 US-10-914A-984231  ALIGNMENTS  FEBULT 1  US-11-262-388-82  FEBULT 3  APPLICANT: Signaevsky, Maxim  TITLE OF INVENTION: Compositions and Methods for Treatmen  TITLE OF INVENTION: Compositions and Methods for Days  FRIDR APPLICATION NUMBER: US 60/415,859  PRIOR FILING DATE: 2002-10-02  PRIOR FILING DATE: 2002-10-02  PRIOR FILING DATE: 2002-10-02  PRIOR FILING DATE: 2003-04-18  NUMBER OF SEQ ID NOS: 91  SEQ ID NO 82  LENGTH: 20	US-11-121-849-39050	Sequence	39050, A
25 13.2 66.0 25 17 US-11-136-527-297166  36 13 65.0 25 17 US-11-136-521-297166  37 13 65.0 25 11 US-10-933-982-120239  39 13 65.0 25 11 US-10-933-982-151912  40 12.8 64.0 12 18 10 US-10-914A-60727  41 12.8 64.0 18 10 US-10-914A-60727  42 12.8 64.0 19 10 US-10-914A-60727  43 12.8 64.0 19 10 US-10-914A-60727  44 12.8 64.0 19 10 US-10-914A-984231  45 12.8 64.0 19 10 US-10-914A-984231  45 12.8 64.0 19 10 US-10-914A-984231  45 12.8 64.0 19 10 US-10-914A-984231  ALIGNMENTS  Publication No. US20060040866A1  Sequence 82, Application US/11262388  Publication No. US20060040866A1  APPLICANT: Rocchi, Palma  APPLICANT: Signaevsky, Maxim  APPLICANT: Signaevsky, Maxim  TITLE OF INVENTION: Compositions and Methods for Treatmen  TITLE OF INVENTION: Compositions and Methods for Treatmen  TITLE OF INVENTION: Compositions and Methods for Treatmen  TITLE OF INVENTION: Cancers  PRIOR PILING DATE: 2003-10-28  PRIOR PILING DATE: 2003-10-02  PRIOR PILING DATE: 2003-10-02  PRIOR FILING DATE: 2003-10-02  PRIOR FILING DATE: 2003-10-02  PRIOR FILING DATE: 2003-10-02  PRIOR FILING DATE: 2003-04-18  NUMBER OF SEQ ID NOS: 91  SEQ ID NO 82  LENGTH: 20	US-11-121-849-143212	Sequence	143212,
c 36 13 65.0 25 11 US-10-333-98-120339 c 38 13 65.0 25 11 US-10-933-982-151912 c 38 13 65.0 25 11 US-10-933-982-151912 39 13 65.0 25 11 US-10-914-60726 c 40 12.8 64.0 18 10 US-10-914A-721661 c 42 12.8 64.0 19 10 US-10-914A-721661 c 43 12.8 64.0 19 10 US-10-110-914A-261943 c 44 12.8 64.0 19 10 US-10-110-914A-261943 c 45 12.8 64.0 19 10 US-10-110-914A-261943 c 45 12.8 64.0 19 10 US-10-110-914A-984231 c 45 12.8 64.0 19 10 US-10-110-914A-984231  RESULT 1 US-11-262-388-82 publication No. US20060040886A1 GENERAL INFORMATION: APPLICANT: Rocchi, Palma APPLICANT: Gladave, Martin APPLICANT: Signaevsky, Maxim TITLE OF INVENTION: Compositions and Methods for Treatmen; TITLE OF INVENTION: Compositions and Methods for CORRERY TELING DATE: 2005-10-28 CURRENT FILING DATE: 2005-10-28 PRIOR PILING DATE: 2002-10-02 PRIOR FILING DATE: 2002-10-02 PRIOR FILING DATE: 2002-10-02 PRIOR FILING DATE: 2002-10-02 PRIOR FILING DATE: 2003-04-18 NUMBER OF SEQ ID NOS: 91 SSOTHMARE PARENTED TO NOS: 91 SSOTHMARE PARENTED TO NOS: 91 SSOTHWARE PARENTED TO NOS: 91	US-11-136-527-297166	Sequence	297166,
c 37 13 65.0 25 11 US-10-333-982-151912 39 13 65.0 25 11 US-10-934-046A-115670 40 12.8 64.0 18 10 US-10-914A-60726 41 12.8 64.0 18 10 US-10-914A-60727 42 12.8 64.0 19 10 US-10-914A-60747 42 12.8 64.0 19 10 US-10-914A-60747 44 12.8 64.0 19 10 US-10-914A-994231 44 12.8 64.0 19 10 US-10-914A-994231 45 12.8 64.0 19 10 US-10-914A-994231 46 12.8 64.0 19 10 US-10-310-914A-994231 47 12.8 64.0 19 10 US-10-310-914A-994231 48 12 12 12 12 12 12 12 12 12 12 12 12 12	US-10-933-982-120239	Sequence	120239,
c 38 13 65.0 25 11 US-10-313-982-201040  c 40 12.8 64.0 25 11 US-10-9144-60726  c 41 12.8 64.0 18 10 US-10-9144-60727  c 42 12.8 64.0 19 10 US-10-914A-60727  c 43 12.8 64.0 19 10 US-10-914A-60727  c 44 12.8 64.0 19 10 US-10-914A-60744  c 44 12.8 64.0 19 10 US-10-914A-984231  c 45 12.8 64.0 19 10 US-10-914A-984231  c 45 12.8 64.0 19 10 US-10-914A-984231  Sequence 82, Application US/11262388  Publication No. US20060040866A1  Sequence 82, Application US/11262388  Publication No. US2006004086A1  Sequence 82, Application US/11262388  Publication NoWHER: US/11/262,388  CURRENT FILING DATE: 2003-10-02  PRIOR FILING DATE: 2003-04-18  NUMBER OF SEQ ID NOS: 91  SSEQ ID NO 82  LENGTH: 20	US-10-933-982-151912	Sequence	151912,
39 13 65.0 25 11 US-10-394-048A-115670  c 40 12.8 64.0 18 10 US-10-310-914A-60726  c 42 12.8 64.0 18 10 US-10-310-914A-721661  c 43 12.8 64.0 19 10 US-10-310-914A-60727  c 44 12.8 64.0 19 10 US-10-310-914A-261943  c 45 12.8 64.0 19 10 US-10-310-914A-261943  c 45 12.8 64.0 19 10 US-10-310-914A-261943  c 45 12.8 64.0 19 10 US-10-310-914A-984231  RESULT 1 US-11-262-388-82  Publication No. US20060040886A1  Sequence 82, Application US/11262388  Publication No. US20060040886A1  GAPPLICANT: Rocchí, Palma  APPLICANT: Signaevsky, Maxim  TITLE OF INVENTION: Cancers  PRICA PAPLICATION NUMBER: US/11/262,388  CURRENT FILING DATE: 2005-10-28  PRIOR PRILING DATE: 2002-10-02  PRIOR PLILNG DATE: 2002-10-02  PRIOR FILING DATE: 2002-10-02  PRIOR FILING DATE: 2002-10-02  PRIOR FILING DATE: 2003-04-18  NUMBER OF SEQ ID NOS: 91  SSOFTWARE PATENTIAN VERSION 3.2  LENGTH: 20	US-10-933-982-201040	Sequence	201040,
C 40 12.8 64.0 18 10 US-10-914A-60726 C 41 12.8 64.0 18 10 US-10-110-914A-60727 C 42 12.8 64.0 19 10 US-10-110-914A-60727 C 43 12.8 64.0 19 10 US-10-110-914A-60744 C 44 12.8 64.0 19 10 US-10-110-914A-60744 C 45 12.8 64.0 19 10 US-10-110-914A-984231 C 45 12.8 64.0 19 10 US-10-310-914A-984231 SEGULT 1 US-11-262-388-82 SEQUENCE 82, Application US/11262388 SPDAICANT: SIGNATION: APPLICANT: Signaevsky, Maxim APPLICANT: Signaevsky, Maxim TITLE OF INVENTION: Compositions and Methods for Treatmen; TITLE OF INVENTION: Compositions and Methods for Treatmen; TITLE OF INVENTION: Compositions and Methods for Treatmen; TITLE OF INVENTION: Compositions and CURRENT FILING DATE: 2005-10-28 FRIOR APPLICATION NUMBER: US/10/605,498 PRIOR APPLICATION NUMBER: US/0605,498 PRIOR APPLICATION NUMBER: US 60/415,859 PRIOR FILING DATE: 2002-10-02 PRIOR PILING DATE: 2002-10-02 PRIOR FILING DATE: 2002-10-02 PRIOR FILING DATE: 2003-04-18 NUMBER OF SEQ ID NOS: 91 SSEQ ID NO 82 LENGTH: 20	US-10-934-048A-115670	Sequence	115670,
c 41 12.8 64.0 18 10 US-10-914A-721661 c 42 12.8 64.0 19 10 US-10-110-914A-60727 c 43 12.8 64.0 19 10 US-10-310-914A-60744 c 44 12.8 64.0 19 10 US-10-310-914A-60744 c 44 12.8 64.0 19 10 US-10-310-914A-984231 c 45 12.8 64.0 19 10 US-10-310-914A-984231  BESULT 1 US-11-262-388-82 Sequence 82, Application US/11262388 Publication No. US20060040886A1 GENERAL INFORMATION: APPLICANT: Rocchi, Palma APPLICANT: Signaevsky, Maxim APPLICANT: Signaevsky, Maxim TITLE OF INVENTION: Cancers FILE REFERENCE: UBC-P-03 TITLE OF INVENTION: Cancers FILE REFERENCE: UBC-0-28 CURRENT APPLICATION NUMBER: US/11/262,388 PRIOR FILING DATE: 2003-10-02 PRIOR PPLING DATE: 2003-10-02 PRIOR APPLICATION NUMBER: US 60/415,859 PRIOR FILING DATE: 2003-10-02 PRIOR PPLING DATE: 2003-10-02 PRIOR APPLICATION NUMBER: US 60/463,952 PRIOR FILING DATE: 2003-10-02 PRIOR FILING DATE: 2003-04-18 NUMBER OF SEQ ID NOS: 91 SSC ID NO 82 LENGTH: 20	US-10-310-914A-60726	Sequence	60726, A
C 42 12.8 64.0 19 10 US-10-914A-60727 C 43 12.8 64.0 19 10 US-10-110-914A-60744 C 44 12.8 64.0 19 10 US-10-310-914A-261943 C 45 12.8 64.0 19 10 US-10-310-914A-261943 C 45 12.8 64.0 19 10 US-10-310-914A-984231  RESULT 1 US-11-262-388-82 Sequence 82, Application US/11262388 Publication No. US20060040886A1 Sequence 82, Application US/11262388 Publication No. US20060040886A1 APPLICANT: Gleave, Martin APPLICANT: Signaevaky, Maxim TITLE OF INVENTION: Compositions and Methods for Treatmen; TITLE OF INVENTION: Compositions and Methods for Treatmen; TITLE OF INVENTION: Cancers FILE REFERENCE: UBC.P-031 CURRENT FILING DATE: 2005-10-28 PRIOR APPLICATION NUMBER: US/11/662,388 CURRENT FILING DATE: 2002-10-02 PRIOR APPLICATION NUMBER: US 60/463,952 PRIOR FILING DATE: 2002-10-02 PRIOR FILING DATE: 2002-10-02 PRIOR FILING DATE: 2002-10-02 PRIOR FILING DATE: 2003-04-18 NUMBER OF SEQ ID NOS: 91 SSCQ ID NO 82 LENGTH 20 LENGTH: 20	US-10-310-914A-721661	Sequence	721661,
c 43 12.8 64.0 19 10 US-10-310-914A-60744  c 44 12.8 64.0 19 10 US-10-310-914A-261943  c 45 12.8 64.0 19 10 US-10-310-914A-261943  c 45 12.8 64.0 19 10 US-10-310-914A-261943  c 45 12.8 64.0 19 10 US-10-914A-984231  ALIGNMENTS  RESULT 1 US-11-562-388-82  S Equence 82, Application US/11262388  Publication No. US2006004086A1  GENERAL INFORMATION: APPLICANT: Signaevsky, Maxim APPLICANT: Signaevsky, Maxim TITLE OF INVENTION: Compositions and Methods for Treatmen; TITLE OF INVENTION NUMBER: US/10/605,498  PRIOR APPLICATION NUMBER: US/0605,498  PRIOR PILING DATE: 2002-10-02  PRIOR APPLICATION NUMBER: US 60/463,952  PRIOR FILING DATE: 2002-10-02  PRIOR FILING DATE: 2003-10-18  NUMBER OF SEQ ID NOS: 91  SSEQ ID NO 82  LENGTH: 20  LENGTH: 20	US-10-310-914A-60727	Sequence	60727, A
c 44 12.8 64.0 19 10 US-10-310-914A-265943 c 45 12.8 64.0 19 10 US-10-310-914A-984231  BEBULT 1 US-11-262-388-82 Sequence 82, Application US/11262388 Publication No. US2006004086A1 GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: Cancers FILE REFERENCE: UBC.P-031 CURRENT APPLICATION NUMBER: US/11/262,388 CURRENT FILING DATE: 2003-10-02 FRIOR FILING DATE: 2003-04-18	US-10-310-914A-60744	Sequence	60744, A
C 45 12.8 64.0 19 10 US-10-914A-984231  RESULT 1 US-11-262-388-82 US-11-262-388-82 Squence 82, Application US/11262388 Publication No. US20060040886A1 Squence 82, Application US/11262388 Publication No. US20060040886A1 GARDERAL INPORMATION: APPLICANT: Signaevaky, Maxim TITLE OF INVENTION: Compositions and Methods for Treatmen; TITLE OF INVENTION WOMBER: US/11/262,388 CURRENT FILING DATE: 2005-10-28 PRIOR APPLICATION NUMBER: US 60/415,859 PRIOR PEDILCATION NUMBER: US 60/415,859 PRIOR APPLICATION NUMBER: US 60/463,952 PRIOR FILING DATE: 2003-10-18 NUMBER OF SEQ ID NOS: 91 SSQ ID NO 82 LENGTH: 20	10-310-914A-2619	Sequence	6194
RESULT 1  US-11-262-388-82  US-11-262-388-82  Publication No. US20060040886A1  GENERAL INFORMATION:  APPLICANT: Rocchi, Palma  APPLICANT: Signaevsky, Maxim  TITLE OF INVENTION: Compositions and Methods for Treatmen;  TITLE OF INVENTION NUMBER: US/10/605,498  PRIOR APPLICATION NUMBER: US/005-10-28  PRIOR APPLICATION NUMBER: US 60/415,859  PRIOR PILING DATE: 2002-10-02  PRIOR FILING DATE: 2002-10-02  PRIOR FILING DATE: 2003-04-18  NUMBER OF SEQ ID NOS: 91  SEQ ID NOS: 91  SEQ ID NO 82  LENGTH: 20	10-310-914A-9842	Sequence	4231
RESULT 1 UG-11-262-388-82 Sequence 82, Application US/11262388 Sequence 82, Application US/11262388 Publication No. US2006004086A1 GENERAL INFORMATION: APPLICANT: Glave, Maxim APPLICANT: Signaevsky, Maxim TITLE OF INVENTION: Compositions and Methods for Treatmen; TITLE OF INVENTION: Cancers TITLE OF INVENTION: Cancers FILE REFERENCE: UBC.P-031 CURRENT APPLICATION NUMBER: US/11/262,388 CURRENT FILING DATE: 2003-10-02 FRIOR FILING DATE: 2003-10-02 PRIOR FILING DATE: 2003-10-02 PRIOR PEPLICATION NUMBER: US 60/415,859 PRIOR FILING DATE: 2003-10-02 PRIOR FILING DATE: 2003-04-18 NUMBER OF SEQ ID NOS: 91 SEQ ID NOS: 91 SEQ ID NO 82 LENGTH 20	ALIGNMENTS		
RESULT 1  BESULT 1  BESULT 1  BEQUENCE 32.388-82  Sequence 82, Application US/11262388  Publication No. US2006004086A1  GENERAL INFORMATION:  APPLICANT: Blave, Martin  APPLICANT: Signesveky, Maxim  TITLE OF INVENTION: Compositions and Methods for Treatmen  TITLE OF INVENTION: Cancers  FILE REFERENCE: UBC.P-031  CURRENT APPLICATION NUMBER: US/11/262,388  CURRENT FILING DATE: 2003-10-02  PRIOR PELING DATE: 2003-10-02  PRIOR APPLICATION NUMBER: US 60/463,952  PRIOR PELING DATE: 2003-04-18  NUMBER OF SEQ ID NOS: 91  SEQ ID NO 82  LENGTHARE PATENTIN VERSION 3.2			
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CURRENT FILING DATE: 2005-10-28 CURRENT FILING DATE: 2005-10-28 PRIOR APPLICATION NUMBER: US/10/605,498 PRIOR FILING DATE: 2003-10-02 PRIOR APPLICATION NUMBER: US 60/415,859 PRIOR FILING DATE: 2002-10-02 PRIOR FILING DATE: 2003-10-18 PRIOR FILING DATE: 2003-04-18 NUMBER OF SEQ ID NOS: 91 SEQ ID NO 82 LENGTH: 20			
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S	U/415,859		
FRIOR AFFLICATION NUMBER: US 60/463,932  NUMBER OF SEQ ID NOS: 91  SOFTWARE Patentin version 3.2  SEQ ID NO 82  LENGTH: 20	000 000		
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Gaps

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20; Conservative

Matches

Query Match Best Local Similarity

TYPE: DNA ORGANISM: Homo sapiens

US-11-262-388-82

Score 20; DB 18; Length 20; Pred. No. 1.9;

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Sequence Sequence Sequence Sequence Sequence

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Sequence 1230089, Sequence 940948, Sequence 1294776

940948, 1294776, 597930,

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ORGANISM: Homo sapiens
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; ORGANISM: Human
US-10-310-914A-649206
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sequence 90, Application US/11262388
publication No. US20060040886A1
geneRAL INPORMATION:
GENERAL INPORMATION:
THORMATION:
APPLICANT: Signaeveky, Maxim
TITLE OF INVENTION: Cancers
TITLE OF INVENTION: Cancers
TITLE OF INVENTION: Cancers
FILE REFERENCE: UBC.P-031
CURRENT APPLICATION NUMBER: US/11/262,388
CURRENT APPLICATION NUMBER: US/10/605,498
PRIOR PILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: US 60/415,859
PRIOR PILING DATE: 2003-10-02
PRIOR PILING DATE: 2003-10-02
PRIOR PILING DATE: 2003-04-18
NUMBER OF SEQ ID NOS: 91
SSOFTWARE: PRECENTION NUMBER: US 60/463,952
PRIOR PILING DATE: 2003-04-18
NUMBER OF SEQ ID NOS: 91
SSOFTWARE: PRECENTION VUMBER: US 60/463,952
FRIOR PILING DATE: 2003-04-18
SSOFTWARE: PRECENTION VUMBER: US 60/463,952
FRIOR PILING DATE: 2003-04-18
SSOFTWARE: PRECENTION VUMBER: US 60/463,952
FRIOR PILING DATE: 2003-04-18
SSOFTWARE: PRECENTION VUMBER: US 60/463,952
FRIOR PILING DATE: 2003-04-18
SSOFTWARE: PRECENTION VUMBER: US 60/463,952
FRIOR PILING DATE: 2003-04-18
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SSOFTWARE: PRECENTION VERSION 3.2
Sequence 81, Application US/11262388

Publication No. US20060040886A1

GENERAL INFORMATION:

APPLICANT: Gleave, Martin

APPLICANT: Rocchi, Palma

APPLICANT: Rocchi, Palma

TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other

TITLE OF INVENTION: Cancers

FILE REFERENCE: UBC, P-031

CURRENT APPLICATION NUMBER: US/11/262,388

CURRENT PILING DATE: 2005-10-28

PRIOR PILING DATE: 2003-10-02

PRIOR FILING DATE: 2003-10-02

SOFTWARE: Patentin version 3.2

LENGTH: 21
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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US-11-262-388-81
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ORGANISM: Homo sapiens
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US-11-262-388-90/c
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RESULT 4 US-11-262-388-3

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Sequence 3, Application US/11262388

Publication No. US20060040886A1

GENERAL INFORMATION:
APPLICANT: Gleave, Martin
APPLICANT: Bocchi, Palma
APPLICANT: Bignaeverky, Maxim
TITLE OF INVERTION: Compositions and Methods for Treatment of Prostate and Other
TITLE OF INVERTION: Cancers
TITLE OF INVERTION: Cancers
FILE REPRENEUE: USC. 10.28
CURRENT FILING DATE: 2005-10-28
FRIOR APPLICATION NUMBER: US 60/415,859
FRIOR APPLICATION NUMBER: US 60/415,859
FRIOR APPLICATION NUMBER: US 60/463,952
FRIOR APPLICATION NUMBER: US 60/463,952
FRIOR APPLICATION NUMBER: US 60/463,952
FRIOR FILING DATE: 2003-04-18
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
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US-10-310-914A-649206/C
US-10-310-914A-649206, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPREMEE: 0607.0200.0200.02003
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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Sequence 405955, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded STITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
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Pred. No. 2e+02;
0; Mismatches 0; Indels
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Pred. No. 4.9e+02;
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76.0%; Score 15.2; D
Best Local Similarity 85.0%; Pred. No. 4.9e
Matches 17; Conservative 0; Mismatches
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Best Local Similarity 100.0%; P.
Matches 16; Conservative 0;
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SOFTWARE: Patentin version 3.3
SEQ ID NO 649206
LENGTH: 22
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APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TTLE OF INVENTION: Beloinformatically detectable group of novel regulatory genes and
TTLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-914A-1294776/c

Sequence 1294776, Application US/10310914A

Sequence 1294776, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION WUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PATENTIN VETSION 3.3
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                                                                                                                                 Indels
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                                                                                  Score 14.8; DB 10;
Pred. No. 7.8e+02;
2; Mismatches 2;
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; Sequence 940948, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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                                                                               Query Match 74.0%;
Best Local Similarity 77.8%;
Matches 14; Conservative
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Matches 15; Conservative
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Matches 15; Conservative
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US-10-310-914A-597930/c
                            US-10-310-914A-1230089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1294776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 940948
LENGTH: 18
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Publication No. US2006004086A1

GENERAL INPORMATION:

APPLICANT: Gleave, Martin

APPLICANT: Gleave, Marxin

TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other

TITLE OF INVENTION: Cancers

FILE REPRENCE: UBC. P-031

CURRENT APPLICATION NUMBER: US/11/262,388

CURRENT FILING DATE: 2003-10-28

PRIOR FILING DATE: 2003-10-02

PRIOR FILING DATE: 2003-04-18

NUMBER OF SEQ ID NOS: 91

SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1230089, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Basinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NOS: 1230089
LENGTH: 23
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Pred. No. 6.3e+02;
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 405955
LENGTH: 25
                                                                                                                                                                                                                                                           Query Match 76.0%; Score 15.2; DB 17; Best Local Similarity 85.0%; Pred. No. 4.8e+02; Matches 17; Conservative 0; Mismatches 3;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                        0; Mismatches
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Best Local Similarity 100.
Matches 15; Conservative
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US-11-262-388-4
                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-405955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-310-914A-1230089
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us-10-605-498-82.rnpbn

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6 GGACGCGGCGGCGGUC
                                                                                                                                            1 GGGACGCGCGCTC 14
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                                          Query Match
Best Local Similarity 92.9
Matches 13; Conservative
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Matches 14; Conservative
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US-10-310-914A-279178
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US-10-310-914A-279178
       US-10-310-914A-185611
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Kvuzat
APPLICANT: Bentwich, Kvuzat
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
Uses thereof
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 940913
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Sequence 185611, Application US/10310914A
Sequence 185611, Application US/10310914A
Sequence 185611, Application US/10310914A
Sequence 185611, Application US/10310914A
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Baniler, Kvuzat
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION UNMERE: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 185611
LENGTH: 22
                                                             APPLICANT: Shiler, Kvazat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1380402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 597930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.0%; Score 14.4; DB 10; 93.8%; Pred. No. 1.2e+03; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGACGCGCGCTCGG 16
Publication No. US2006003322A1
GENERAL INFORMATION:
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Best Local Similarity 93.8
Matches 15; Conservative
                                             APPLICANT: Bentwich, Isaac
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US-10-310-914A-597930
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ORGANISM: Human
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US-10-310-914A-279177, Application US/10310914A
| Sequence 279177, Application US/10310914A
| Publication No. US20060003322A1
| Sequence 279177, Application No. US2006000332A1
| Publication No. US2006000332A1
| GENERAL INFORMATION
| APPLICANT: Bantwich, Isaac
| APPLICANT: Shiler, Kvuzat
| TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
| TITLE OF INVENTION: uses thereof
| TITLE REPERENCE: 06097, 0200. CPUSO1
| CURRENT APPLICATION NUMBER: US/10/310, 914A
| CURRENT FILING DATE: 2002-12-06
| WUMBER OF SEQ ID NOS: 1388402
| SOFTWARE: Patentin version 3.3
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE REFERENCE: 06007-10200.CPUSO1
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOOFWARE: Patentin version 3.3
SEQ ID NO 279178
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Score 14; DB 10; Length 22;
Pred. No. 2e+03;
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Pred. No. 2.5e+03;
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Pred. No. 2.5e+03;
1; Mismatches 2;
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                                               1; Mismatches
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82.4%;
  70.0%;
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Best Local Similarity 82.4%;
Matches 14; Conservative
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yz20q11.rl

OM nucleic

Run on:

Sequence:

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AZ513847 IM00360D0
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AZ769255 IM0569B17
AJ746842 AJ746842
CZ472687 G02234-5p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF131807 32 bp mRNA linear EST 24-OCT-2000
601820724F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052596 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:4052596"
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/tiab.host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC_58"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5,
and 3' adaptors were used in cloning as follows: 5,
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGGAGCAGATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGGGCAGATATGGCC-3' and 3' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E 1 (bases | Houo.)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Prayad by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LiCM889 row: p column: 05

High quality sequence start: 8

High quality sequence stop: 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                              CZ472687
CZ488898
                 CG724391
N55046
                                                   AZ346691
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                                                                                                                                                                                CZ472135
                                                                                                                                                                                               AA912813
BI915569
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                                                                                                                                                                                                                                   911196
                                                                                                                                                             31101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nRNA sequence.
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$52.0
$52.0
$52.0
$52.0
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$52.0
$50.0
$50.0
$50.0
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RESULT 1
BF131807/c
LOCUS
DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
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AA867755 vx16508.r
CZL69504 G050C04 G
AZ826864 2M0102H20
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CF28077 TEAF--01
CF642505 D52 E05 F
CR642505 D52 E05 F
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                                                                                                                 8, 2006, 09:37:03 ; Search time 1958 Seconds (without alignments) 477.907 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
             GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                             78772
                                                                                                                                                                                                                                                                                                                       41078325 seqs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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CG731752
TA103C01P
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seq length: 35
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Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submitseion
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
S., Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail:Kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
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                                                                                                                                                                                                                                                                                                     AG203073 26 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-087B01.T7, genomic survey
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PGR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA).
                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes (chimpanzee)
Ban troglodytes
Eukaryota, Ometazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                            Gaps
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/clone_lib="RP-43 Chimpanzee Male BAC Library"
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                                                                                                     64.0%; Score 12.8; DB 2;
87.5%; Pred. No. 2.5e+05;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pan troglodytes"
/mol type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-087B01.T7"
/sex="male"
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GSS.
                                                                                                                                                                                                 27 CGCTGCGCTCGGTCGT 12
                                                                                                                                                                           S CGCGGCGCTCGGTCAT 20
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Best Local Similarity
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A1287864/c
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AG203073
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A1287864
28 bp mRNA linear EST 24-NOV-1998
qv07012.x1 NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:1980887 3'
similar to SW:CA44 HUMAN P53420 COLLAGEN ALPHA 4 (IV) CHAIN
PRECURSOR. ;contains MER22.b3 TAR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi, Muroidea; Muridae; Mus.
1 (bases 1 to 31)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:1980887"
/tissue_type="IMAGE:1980887"
/lab_host="DH108"
/clone_lib="NCI CGAP_Kid8"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.2 kb. Life Technologies catalog #:
11524-014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CGAP),
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarhini,
                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.
1 (bases 1 to 28)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
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Seg primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Mus musculus
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                                                                                                                                                                                                                                            Homo sapiens (human)
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Unpublished (1997)
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Musmanla; Butheria; Burheria; Burniae; Murinae; Mus.

Sciurognathi; Muroidea; Murinae; Mus.

E 1 (bases 1 to 31)

S Dunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Menen,B., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah

University of Utah
                                                Bmail: info@genetrap.de
UJCEO gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
clone_id=G050C04' ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
'l Inhouse Sequence Identifier: 16629
Class: Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALGEBERG 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0102H20 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell type="Embryonic stem cell"
/cell_line="ES cells [C57BL/63 x 129S6/SvEvTac] F1"
/clone_lib="GGTC Gene Trap Library GV07C05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.0%; Score 12; DB 10; Length 31; 75.0%; Pred. No. 5.7e+05; ive 0; Mismatches 5; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: H column: 20
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
                               German Genetrap Consortium (GGTC)
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="G050C04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: U3CEO"
                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Conservative
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Fax: 801 585 7177
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31 bp mRNA linear GSS 22-MAR-2005 G0550C04 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone G050C04, mRNA sequence.
CZ169504
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Hansen, J., Flose, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
Arnold, H.H., Schnutger, F., Wurst, W., von Melchner, H. and Ruiz, P.
A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
Proc. Natl. Acad. Sci. Us.A. 100 (17), 9918-9922 (2003)
On Mar 22, 2005 this sequence version replaced gi:58224102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                         Unpublished (1996)
Contact: Marra MyNouse EST Project
Washl-HPMI Mouse EST Project
Washlngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1264599"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                             MGI:667151
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15 Balzergue, S.
16 Balzergue, S.
17 Submission
18 Submission
19 
                                                                                                                                                                                                                                        Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared bNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM92 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana T-DNA flanking sequence, left border, clone 339810, genomic survey sequence.
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T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 1.1e+06;
0; Mismatches 1;
                       /clone="UUGC2M0102H20"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
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/db xref="vazon:148305"
/db xref="vazon:148305"
/clone="mgmy006xA17"
/sex="marl-2" hermaphrodite"
/clone="lib="marl-2" hermaphrodite"
/clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD028820 31 bp mRNA linear BST 07-MAY-2003 mgmy006xA17f.b Magnaporthe grisea MY Uni-Zap XR Library Magnaporthe grisea cDNA clone mgmy006xA17 5', mRNA sequence.
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                                                                                                                                                /clone="339B10"
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Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Pungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
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Chromatogram file of this sequence is available, see contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 23;
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Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.0%; Score 11.2; DB 10;
81.2%; Pred. No. 1.4e+06;
ative 0; Mismatches 3;
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                1. .23
/note="T-DNA flanking sequence
left border"
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/organism="Magnaporthe grisea"
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                                                                                                                                                                                                                                                  /ecotype="Wassilewskija"
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/strain="70-15"
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Submitted (23-007-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
FR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequence from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                            AJ599957 33 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ599957.1 GI:37949585
GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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100.0%; Pred. No. 1.6e+06;
tive 0; Mismatches 0; Indels
                                                                                     Length 21;
                                                                                                                                         0; Indels
        and selected for ampicillin resistance."
                                                                               55.0%; Score 11; DB 9; Le
100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
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EMBO Rep. 3 (12), 1152-1157 (2002)
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Balzergue, S.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                 GSS 03-OCT-2000
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                                                                                                                                                                                                                                                                                                                                           AZ420773 21 bp DNA linear GSS 03-OCT-200
1M0198E18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Musinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunn, D., Aoyagi, A., Barber, M.; Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                             Gaps
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                                                         Length 31;
                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                         clone UUGC1M0198E18 R, genomic survey sequence. AZ420773
                                                 56.0%; Score 11.2; DB 6;
81.2%; Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0198 row: E column: 18
                                                                                                        0; Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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mol_type="genomic DNA"
strain="C57BL60"
db_xref="taxon:10090"
/clone="tudGCIM0198E18"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                                                                                                        13; Conservative
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Fax: 801 585 7177
                                              Query Match
Best Local Similarity
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84112, USA
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KEYWORDS
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AZ420773/c
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ORIGIN
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION

us-10-605-498-82.rst

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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Dife Technologies, Inc.
CDNA Library Preparation: Dife Seq Lennon, Ph.D.
DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF643223 25 Dp mRNA linear EST 02-OCT-2003
D61_D08 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I (bases 1 to 25)
Nugent, K.G., Choffe, K. and Saville, B.J.
Gene expression during Ustilago maydis diploid filamentous growth:
EST library creation and analyses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clome_lib="NCI_CGAP_Utl"

//otoe="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sal1;
//tote="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Shot; Cloned undirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Eukaryota, Fungi, Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:2286740"
/tissue_type="well-differentiated endometrial
adencearcinoma, 7 pooled tumors"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www-bio.llnI.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 race considered overall poor quality

    .25
    /organism="Homo sapiens"

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High quality sequence stop: 1.
Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                                                                                           Hominidae; Homo.
1 (bases 1 to 25)
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Best Local Similarity 76.5
Matches 13; Conservative
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CF643223/c
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25 bp mRNA linear EST 23-JUN-1999
ty94c11.x1 NCI CGAP_Utl Home sapiens cDNA clone IMAGE:2286740 3'
similar to TR:Q64371 Q64371 PR-VBETA1. ;contains element TAR1
repetitive element ;, mRNA sequence.
AA259780 34 bp mRNA linear EST 18-MAR-1997 va87b10.rl Soares mouse 3NME12 5 Mus musculus cDNA clone LMGE:746395 5' similar to TR:G971986 G971986 NADH DEHYDROGENASE ;,
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Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Sciurognathi; Muroidae; Muridae; Musinae; Mus

1 (bases 1 to 34)

Marra, M.; Hillier, L.; Allen, M.; Bowles, M.; Dietrich, N.; Dubuque, T Geisel, S.; Kucaba, T.; Lacy, M.; Le, M.; Martin, J.; Morris, M.; Schellenberg, K.; Sreptoe, M.; Tan, F.; Underwood, K.; Moore, B.; Theising, B.; Wylie, T.; Lennon, G.; Soares, B.; Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngron University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
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Possible reversed clone: similarity on wrong strand
Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="fetus"
/dev_stage="12.5dpc total fetus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .34
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xrain="taxon:10090"
/clone="IMAGE:746395"
                                                                                                                                                                         Mus musculus (house mouse)
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                                                                       mRNA sequence.
AA259780
AA259780.1 GI:1896266
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Matches 14; Conserv
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FEATURES

Query Match

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RESULT 12 AI758887

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Gaps

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53.0%; Score 10.6; DB 6; 76.5%; Pred. No. 2.5e+06;
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                                                                                                                                                        / .25
/organism="Ustilago maydis"
/mol type="mRNA"
/mol type="mRNA"
/strain="FBB12"
/db xref="taxon:5270"
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/clone lib="Filamentous Forced Diploid"
/note="Vector: pSport; mRNA was extracted from diploid
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II cDNA Library Construction Kit."
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/note="Vector: pSport; mRNA was extracted from diploid
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II cDNA Library Construction Kit."
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D62_B05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
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Ustilago maydis
Bukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Bukaryota; Pungi; Basidiomycota; Ustilaginaceae; Ustilago.
1 (Dases 1 to 29)
Nugent, K.G., Choffe, K. and Saville, B.J.
Nugent expression during Ustilago maydis diploid filamentous growth:
EST library creation and analyses
Fungal Genet. Biol. 41 (3), 349-360 (2004)
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6,
Tel: 905 569 4702
Fax: 905 828 3792
Email: beaville@utm.utoronto.ca
Email: beaville@utm.utoronto.ca
Plate: UTM-UM-0126/7-062-UTM row: 05 column: B
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGGG 3')
High quality sequence stop: 29.
                                                    Fasi: boscille@utm.utoronto.ca
Plate: UTM-UM-D126/7-061-UTM row: 08 column: D
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGGG 3')
High quality sequence stop: 25.
Location/Qualifiers
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Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for
Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for
Developmental Biology, Laboratory for Morphogenetic Singaling;
Developmental Biology, Laboratory for Morphogenetic Singaling;
(Enail:shayashi@cdb.riken.go.jp, Tel:81-78-301-3184,
Fax:81-78-301-3183)
This clone was isolated from genomic DNA flanking an insertion of
the Pelement vector P(GawB) of a Drosophila strain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aigaki,T., Matsuzaki,F., Taniguchi,M., Akimoto,A., Takeuc. Aigaki,T., Matsuzaki,F., Nakagoshi,H., Tanimura,T., Ueda,R., Uemura,T., Yoshihara,M. and Goto,S.
GBTDB, a database compiling expression patterns and molecular locations of a collection of Gal4 enhancer traps
2 (bases 1 to 33)
Hayashi.S.
                                                     Gaps
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Bukaryota, Metazoa, Arthropoda, Haxapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila
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/chromosome="2"
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/loone="NR1197-5-1"
/note="flanking P{GaWB} transposon insertion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 33;
Length 29;
                                                     Indels
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                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster DNA, clone:NP1197-5-1, transposon insertion, genomic survey sequence.
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Pred. No. 2.4e+06;
                                                     0; Mismatches
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/strain="NP1197"
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25195, A 49392, A 3, Appli 4, Appli 45, Appli 46, Appli 47, Appli 47, Appli 6, Appli 13, Appli 2, Appli 2, Appli 3, Appli 4, Appli 4, Appli 6, Appli 7, Appli 7, Appli 7, Appli 8, Appli 8, Appli 7, Appli 11, Appli 7, Appli 8, Appli 11, Appli

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GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Gaguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT PILING DATE: 2001-10-12
PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.0%; Score 14.2; DB 3; Length 33; 84.2%; Pred. No. 3e+03;
US-09-158-863C-38
US-09-589-560B-58
US-09-396-196C-25195
US-09-396-196C-49392
US-09-487-58B-3
US-09-467-671-1
US-08-485-355B-4
US-09-045-583-45
US-09-045-583-45
US-09-045-583-44
US-09-534-185-45
US-09-534-185-44
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US-09-910-133
US-08-910-158-13
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Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: AFFINENT: David Mack
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CHRENT FILING DATE: 1999-09-15
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
                                                                                                                                                                                                                                                                                                                                                                           US-09-942-588A-31
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 33
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Sequence 42173, A
Sequence 46323, A
Sequence 46335, A
Sequence 46335, A
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Appl
Sequence 8773, Ap
Sequence 35, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 35, Appl
Sequence 52, Appl
Patent No. 5240848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Appl
Sequence 9, Appli
Sequence 41065, A
Sequence 46162, A
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Sequence 9, Appli
Sequence 16, Appl
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370.325 Million cell updates/sec
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               GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                       May 8, 2006, 09:47:57; Search time 96 Seconds
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
/cgn2_6/ptodata/1/ina/PCOMB.seq:*
/cgn2_6/ptodata/1/ina/PCOMB.seq:*
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US-09-396-196G-46323
US-09-396-196G-46323
US-09-396-196G-46323
US-09-396-196G-46335
US-09-396-196G-53301
US-09-450-515-19
US-10-131-827-8773
US-10-131-827-8773
US-10-131-827-8773
US-09-540-014-35
US-09-540-014-35
US-09-540-014-35
US-09-396-196G-40648
US-09-396-196G-40648
US-08-474-633A-16
US-08-474-633A-16
US-08-823-771-16
US-08-823-771-16
US-08-936-196G-41065
US-09-396-196G-41065
US-09-396-196G-41065
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                                                                                                                                                                                                                                                                                                                                 1303057 seqs, 888780828 residues
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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seq length: 35
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                                                                                                                                                                                    70.0%; Score 14; DB 3; Length 25; 100.0%; Pred. No. 3.8e+03; tive 0; Mismatches 0; Indels
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US-09-396-196G-46323/C
i Sequence 46323, Application US/09396196G
i Patent No. 6821724
i GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
ITILE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: EsatSEQ for Windows Version 4.0
SEQ ID NO 46323
LENGTH: 25
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Sequence 46324, Application US/09396196G

Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: AFFWHETEX, Inc.
FILLE OF INVENTION: Methods of Genetic Analysis
FILE PERRENCE: 3101.1
CURRENT PLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
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PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42173
LENGTH: 25
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46324
LENGTH: 25
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                         Best Local Similarity 100.
Matches 14; Conservative

// ORGANISM: mus musculus
US-09-396-196G-46323
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US-09-396-196G-46324
                                                                                                                        ORGANISM: Mus musculus
                                                                                                                                             US-09-396-196G-42173
                                                                                                                                                                                      Query Match
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Query Match 69.0%; Score 13.8; DB 3;
Best Local Similarity 88.2%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                     Sequence 46335, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Mack
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-396-196G-53301
; Sequence 53301, Application US/09396196G
; Parent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.0%; Score 13.8; DB 3; Best Local Similarity 88.2%; Pred. No. 4.6e+03; Matches 15; Conservative 0; Mismatches 2;
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Pred. No. 8.3e+03;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53301
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GACGCGCGCTCGGTCAT 20
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                                                                                                4 ACGCGCCCTCGGTCAT 20
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                                                                                                                                          19 ACGCTGCGCACGGTCAT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 ACGCTGCGCACGGTCAT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 66.0%;
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-53301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: mus musculus US-09-396-196G-46335
                                                                                                                                                                                                                     RESULT 5
US-09-396-196G-46335/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/10206654
Patent No. 6919493
GENERAL INFORMATION:
APPLICANT: Rodriguez, Raymond L.
APPLICANT: Rodriguez, Raymond L.
ITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
ITILE OF INVENTION: IN ALPHA-AMYLASE GENES
           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/450,515
FILING DATE: 29-No. 6680425-1999
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/046,858
FILING DATE: -UNknown>
ATTORNEY/AGENT INFORMATION:
NAME: Deblinger: Peter J.
REGISTRATION NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 28,006
TELLEPAX: 650-324-0960
TELLEFAX: 650-324-0960
TELLERAX: 650-324-0960
TELLERAX: 650-324-0960
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TELLERAY: 650-324-0960
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APPLICATION NUMBER: US/10/206,654
FILING DATE: 25-011-2002
CLASSIFICATION: UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/046,858A
FILING DATE: 24-MAR-1998
APPLICATION NUMBER: 00/042,376
ATTORKST/AGENT INPORMATION:
NAME: Dehlinger, Peter J.
REGISTRATION NUMBER: 28,006
REFERRATION NUMBER: 28,006
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ADDRESSEE: Dehlinger & Associates
STREET: PO Box 60850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
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TELEFAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 19:
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Best Local Similarity 100.0
....hes 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-09-450-515-19
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US.09-450-515-19
US.09-450-515-19
Sequence 19, Application US/09450515
Patent No. 6680425
GENERAL INFORMATION:
APPLICANT: Rodriguez, Raymond L.
TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
TITLE OF INVENTION:
                                    Sequence 19, Application US/09046858A
Patent No. 6048973
GENERAL HYPORMATION: ROTAGE RAYMOND L.
APPLICANT: ROSTIGUEZ, RAYMOND L.
TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
TITLE OF INVENTION: IN ALPHA-AMYLASE GENES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      ZOUNTING USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: DESCRIPTION
SOFTWARE: FASTSED for Windows Version 2.0
CURRAY APPLICATION DATA:
APPLICATION NUMBER: US/09/046,858A
FILING DATE: 24-MAR-1998
CLASSIFICATION NUMBER: 60/042,376
FILING APPLICATION DATA:
APPLICATION NUMBER: 60/042,376
FILING DATE: 24-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dehlinger, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13; DB 3;
Pred. No. 1e+04;
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ADDRESSE: Dehlinger & Associates
STREET: PO Box 60850
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                             ADDRESSEB: Dehlinger & Associates STREET: PO Box 60850 CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Dehlinger, Peter J.
REGISTRATION NUMBER: 28,006
REFRENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEPAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GACGCGCGCTCG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
US-09-046-858A-19
              JS-09-046-858A-19
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US-09-164-210-12/c
; Sequence 12, Application US/09164210
; Betent No. 6. Application US/09164210
; Betent No. 6. Application US/09164210
; GENERAL INFORMATION:
; APPLICANT: P. G. Lemaux et al.;
; TILE OF INVENTION: Production of proteins in plant seeds
; FILE REFERENCE: 48722
; CURRENT FILING DATE: 1998-09-30
; EARLIER APPLICATION NUMBER: 09/164,210
; BARLIER FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                   Length 24;
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                                                                                                                                                                                                                                                                                                                                                                   4; Indels
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CURRENT APPLICATION NUMBER: US 60/126,736

PRIOR PLING DATE: 1999-03-29

PRIOR FILING DATE: 1999-03-31

PRIOR PLING DATE: 1999-03-31

PRIOR PLING DATE: 1999-03-31

PRIOR FILING DATE: 1999-12-06
                                                                                                                                                                                                                                                                                                                Score 12.6; DB 3;
Pred. No. 1.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.0%; Score 12.6; DB 3; Best Local Similarity 78.9%; Pred. No. 1.5e+04; Matches 15; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
PRIOR APPLICATION NUMBER: US 60/177,739
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09538864
; Patent No. 6784346
; GENERAL INFORMATION:
APPLICANT: Cho, Mycong-Je
APPLICANT: Lemaux, Peggy G.
APPLICANT: Buchanan, Bob B.
APPLICANT: Mong, Joshua
APPLICANT: Marx, Corina
                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGACGCGCCCTCGGTCAT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGACGCGCGCTCGGTCAT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                             Query Match 63.0%;
Best Local Similarity 78.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                     ; OTHER INFORMATION: primer US-09-540-014-35
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US-09-538-864-14/c
                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                  FEATURE:
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Sequence 873, Application US/10131827

Setent No. 6905827

GENERAL INFORMATION:

APPLICANT: Woolygemuth, Jay

APPLICANT: Fry, Kirk

APPLICANT: Pry, Kirk

APPLICANT: Woodward, Robert

APPLICANT: Woodward, Robert

APPLICANT: By, Mgoc

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

FILLE REFERENCE: 506612000120

CURRENT PLILING DATE: 2002-09-06

PRIOR FILING DATE: 2001-06-08

PRIOR FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOSS: 9990

SOPTWANDED: DEFORTER CONTINES OF SEQ ID NOSS: 9990

SOPTWANDED: DEFORTER CONTINES OF SEQ ID NOSS: 9990
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                                                                                                                                                                                                       Query Match 65.0%; Score 13; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 1e+04; Matches 13; Conservative 0; Mismatches 0; Indels
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Patent No. 6380372
GENERAL INFORMATION:
APPLICANT: Cho, Mysong-Je
APPLICANT: Calllau, Maxime
APPLICANT: Calllau, Maxime
APPLICANT: Lemauz, Peggy G.
APPLICANT: Lemauz, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: Barley Gene for Thioredoxin and
TITLE OF INVENTION: Barley Gene for Thioredoxin and
TITLE OF INVENTION: NADP-Thioredoxin Reductase
FILE REFERENCE: 2001-0701.30
CURRENT APPLICATION NUMBER: US/09/540,014
CURRENT FILING DATE: 2000-03-31
PRIOR FILING DATE: 1999-03-13
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 2000-01-21
                  LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-206-654-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGACGCGCGCTCGGTCAT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Human cytomegalovirus
US-10-131-827-8773
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
SEQ ID NO 8773
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                           2 GACGCGCGCTCG 14
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Best Local Similarity 78.99
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gequence 35, Application us/loughstham between No. 633493
GENERAL INFORMATION:
APPLICANT: Cho, Myeong-Je
APPLICANT: Caillau, Maxime
APPLICANT: Caillau, Maxime
APPLICANT: Lemanar, Beggy G.
APPLICANT: Lemanar, Bob B.
TITLE OF INVENTION: BARLEY GENE FOR THIOREDOXIN AND TITLE OF INVENTION: NADP-THIOREDOXIN REDUCTASE
FILE REFERENCE: 416272001410
CURRENT APPLICATION NUMBER: US/10/091, 841A
CURRENT APPLICATION NUMBER: US 09/540,014
PRIOR APPLICATION NUMBER: US 00/127,198
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1999-03-31
PRIOR PILING DATE: 2000-01-21
PRIOR PRILICATION NUMBER: US 60/177,740
PRIOR PILING DATE: 2000-01-21
PRIOR PELING DATE: 2000-01-21
PRIOR PELING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
LENGTH: 24
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,739
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEGO ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35, Application US/10091841A
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGACGCGCGCTCGGTCAT 20
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                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 78.9°
Matches 15; Conservative
                                                                                                                                                                                                                                              FEATURE:
CTHER INFORMATION: primer
US-09-538-864-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Primer US-10-091-841A-35
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-US-09-196-196G-40648/c
-: Sequence 40648, Application US/09396196G
-: Patent No. 6821724
-: GENBEAL INFORMATION:
-: APPLICANT: Michael Mittmann

```
## APPLICANT: David Mack
### APPLICANT: David Mack
### APPLICANT: David Lockhart
### APPLICANT: David Lockhart
### APPLICANT: Affymetrix, Inc.
### TITLE OF INVENTION: Methods of Genetic Analysis
### FILE REFERENCE: 310.1.
### CURRENT APPLICATION NUMBER: US/09/396,196G
### CURRENT APPLICATION NUMBER: 06/100,678
### FILING DATE: 1999-09-15
### PRIOR PILING DATE: 1999-09-15
### PRIOR PILING DATE: 1999-09-15
### PRIOR FILING DATE: 1999-09-19
### PRIOR FILING DATE: 1999-19
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